

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 22, 2004, 11:49:33 ; Search time 36 Seconds
(without alignments)
2164.805 Million cell updates/sec

Title: US-10-620-049-23

Sequence: 1 DQMTQTSLSLASLGDRVT.....GLIRYAMDYWGQGTSTVSS 247

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 segs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: sp archaea:*
2: sp bacteria:*
3: sp fungi:*
4: sp human:*
5: sp invertebrate:*
6: sp mammal:*
7: sp mhc:*
8: sp organelle:*
9: sp phage:*
10: sp plant:*
11: sp rodent:*
12: sp virus:*
13: sp vertebrate:*
14: sp unclassified:*
15: sp viirus:*
16: sp bacteriaph:*
17: sp archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	535	40.6	614	11	Q7MT6 mus musculu
2	524.5	39.8	234	11	Q91WP8 mus musculu
3	486	36.9	111	11	Q9DPB8 mus musculu
4	483.5	36.7	110	11	Q9UL83 mus musculu
5	480.5	36.5	233	11	Q91WS9 mus musculu
6	478	36.3	474	11	Q8R3H6 mus musculu
7	471	35.8	142	11	Q924Q1 mus musculu
8	470	35.7	481	11	Q91WT1 mus musculu
9	469.5	35.6	145	11	Q924Q6 mus musculu
10	465.5	35.3	145	11	Q924Q9 mus musculu
11	464.5	35.3	145	11	Q924R1 mus musculu
12	464.5	35.3	145	11	Q924R4 mus musculu
13	463.5	35.2	118	11	Q921C4 mus musculu
14	462.5	35.1	234	11	Q924Q3 mus musculu
15	461	35.0	146	11	Q924Q3 mus musculu
16	459.5	34.9	482	11	Q8K172 mus musculu

17	458.5	34.8	145	11	Q924P7 mus musculu
18	458	34.8	473	11	Q90BL4 mus musculu
19	456.5	34.7	143	11	Q924R0 mus musculu
20	455.5	34.6	488	11	Q8K0F2 mus musculu
21	454	34.5	140	11	Q924R2 mus musculu
22	452	34.3	146	11	Q924R8 mus musculu
23	450.5	34.2	613	11	Q8VCX7 mus musculu
24	449.5	34.1	143	11	Q924Q0 mus musculu
25	446	33.9	117	11	Q90XB9 mus musculu
26	446	33.9	480	11	Q8K0Z4 mus musculu
27	445.5	33.8	473	11	Q90L25 mus musculu
28	444	33.7	168	11	Q9VDC9 mus musculu
29	440.5	33.4	143	11	Q924P9 mus musculu
30	440	33.4	140	11	Q924P8 mus musculu
31	439.5	33.4	137	11	Q924R6 mus musculu
32	439	33.3	146	11	Q924Q8 mus musculu
33	436.5	33.1	141	11	Q924Q4 mus musculu
34	436.5	33.1	463	11	Q991C4 mus musculu
35	436	33.1	142	11	Q924Q2 mus musculu
36	435.5	33.1	145	11	Q924Q7 mus musculu
37	435	33.0	144	11	Q924P5 mus musculu
38	433.5	32.9	136	11	Q7PPE3 mus musculu
39	433	32.9	470	11	Q7TWK1 mus musculu
40	432.5	32.8	110	11	Q9J177 mus musculu
41	431.5	32.8	143	11	Q924P6 mus musculu
42	430.5	32.7	145	11	Q924R3 mus musculu
43	429.5	32.6	143	11	Q924Q5 mus musculu
44	428.5	32.5	143	11	Q924R7 mus musculu
45	428.5	32.5	243	11	Q7QW2 mus musculu

ALIGNMENTS

RESULT 1					
ID	Q7MT6	PRELIMINARY;	PRT;	614	AA.
AC	Q7MT6				
DT	01-OCT-2003 (TRENBLREL. 25, Created)				
DT	01-OCT-2003 (TRENBLREL. 25, Last sequence update)				
DT	01-OCT-2003 (TRENBLREL. 25, Last annotation update)				
DE	Hypothetical protein.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.				
OX	NCBI_TaxId=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;				
RX	MEDLINE=22388257; PubMed=12477937;				
RA	Steinberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,				
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,				
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,				
RA	Hopkins R.F., Jordan R., Moore T., Wax S.I., Wang J., Hsieh F.,				
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,				
RA	Brownstein M.J., Ueda T.B., Toshitoki S., Carinici P., Prange C.,				
RA	Raha S.S., Loguella N.A., Peters G.J., Abramson R.D., Mullaly S.J.,				
RA	Bohak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				
RA	Richards S., Wortley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,				
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,				
RA	Falley J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,				
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,				
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buttefield Y.S.,				
RA	Krzywinski M.I., Skalska U., Small D.E., Scherch A., Schein J.E.,				
RA	Jones S.J., Mair M.A.,				
RT	"Generation and initial analysis of more than 15,000 full-length human				
RT	and mouse cDNA sequences."				
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;				

RA Strausberg R.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC053409; AAH53409.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 614 AA; 67746 MW; 839BAP3B8D124F89 CRC64;

Query Match 40.6%; Score 535; DB 11; Length 614;
 Best Local Similarity 82.9%; Pred. No. 8.3e-37;
 Matches 102; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

QY 125 GGGSEVVOLOQSGPELVKPGASVYKISCKDGYAFNSGMMWVVKORPGGLEWIGRIYPDGG 184
 DB 16 GVASQVQLOQSGPELVKPGASVYKISCKASGYAFSSMMWVVKORPEKGLEWIGRIYPDGG 75

QY 185 DSNYNGKFEKALITLADKSSSTAYVQSLTSVDSAVYFCARSGLRVANDYWGOSTSVT 244
 DB 76 DTVYNGKFKKALITLADKSSSTAYVQSLTSVDSAVYFCARDYGSYFAVWGOSTLVT 135

QY 245 VSS 247
 DB 136 VSA 138

RESULT 2

Q91WF8 PRELIMINARY; PRT; 234 AA.

AC Q91WF8; 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon;
 RA Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC015292; AAH15292.1; -
 DR GO: GO:0005622; C:intracellular; IEA.
 DR GO: GO:0005840; C:ribosome; IEA.
 DR GO: GO:0003735; F:structural constituent of ribosome; IEA.
 DR GO: GO:0006412; F:protein biosynthesis; IEA.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR InterPro: IPR001865; Ribosomal_S7.
 DR Pfam: PF00047; IG; 2.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS00835; IG_LIKE; 2.
 DR PROSITE: PS00290; IG_MHC; 1.
 DR PROSITE: PS00962; RIBOSOMAL_S7_1; 1.
 DR Hypothetical protein.
 SQ SEQUENCE 234 AA; 25929 MW; B0D0B0BEB7812D2 CRC64;

Query Match 39.8%; Score 524.5; DB 11; Length 234;
 Best Local Similarity 52.0%; Pred. No. 1.9e-36;
 Matches 116; Conservative 12; Mismatches 44; Indels 51; Gaps 4;

QY 1 DIQWTTTSSASLGRVYVSCASADIRYLNWYKORPDGTYKPIYTTSLQGVPS 60
 DB 21 DIQWTTTSSASLGRVYVSCASADIRYLNWYKORPDGTYKPIYTTSLQGVPS 80

QY 61 RFGSGSGGTDTSLTINNLEQEDIGTYFCQOGNTPPMTFPGGTGKLEIRGGSGSDGGSGG 120
 DB 81 RFGSGSGGTDTSLTINNLEQEDIGTYFCQOGNTPPMTFPGGTGKLEIRGGSGSDGGSGG 128

QY 121 GGGSGGGSEVVOLOQSGPELVKPGASVYKISCKDGYAFNSGMMWVVKORPGGLEWIGRIY 180
 DB 129 --ADAAPVTSIFPPSSQDLSYGASV-----VCFINNFY 160

QY 181 PG-----DGSNNGKFEKALITLADKSSSTAYVQSLTS 215
 DB 161 PKDINWVKKIDGSERGQGVANS---WTDQOSKOSTYSMSSTLT 200

RESULT 3

Q9D9B8 PRELIMINARY; PRT; 111 AA.

AC Q9D9B8; 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Adult male testis cDNA, RIKEN full-length enriched library,
 clone:1700110L1, full insert sequence.
 DE Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kouchava H.,
 RA Kuehl P., Lewis S., Matsuo Y., Mikaido I., Pesole G., Quackenbush J.,
 RA Schiml L.M., Steubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Batdarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carinci P., de Bonard M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima U., Mazzarelli U., Mombaetis P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohzuki S.,
 RA Hayashizaki Y.;
 RA "Functional annotation of a full-length mouse cDNA collection."
 RT Nature 409:685-690(2001).
 RL EMBL: AK007163; BAB24877.1; -
 DR HSP: P01810; 2FBJ.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; IGV; 1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS00835; IG_LIKE; 1.
 DR PROSITE: PS00962; RIBOSOMAL_S7_1; 1.
 SQ SEQUENCE 111 AA; 11976 MW; 874DFF7BD98BD7B2 CRC64;

Query Match 36.9%; Score 486; DB 11; Length 111;
 Best Local Similarity 90.2%; Pred. No. 1.3e-33;
 Matches 92; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 125 GGGSEVVOLOQSGPELVKPGASVYKISCKDGYAFNSGMMWVVKORPGGLEWIGRIYPDGG 184
 DB 3 GVASQVQLOQSGPELVKPGASVYKISCKASGYAFSSMMWVVKORPEKGLEWIGRIYPDGG 62

QY 185 DSNYNGKFEKALITLADKSSSTAYVQSLTSVDSAVYFCAR 226
 DB 63 DTVYNGKFKKALITLADKSSSTAYVQSLTSVDSAVYFCAR 104

RESULT 4

Q9JL83 PRELIMINARY; PRT; 110 AA.

AC Q9JL83; 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Anti-myosin immunoglobulin heavy chain variable region
 (Fragment).

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BAJB/c;
RX MEDLINE=20448942; PubMed=10922486;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-cell-dependent antibody response to the dominant epitope of
streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
with cardiac myosin.";
RT Infect. Immun. 68:5803-5808 (2000).
DR EMBL; AF206023; AAF69321.1; -.
DR HSSP; P01810; 2FRJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT 110 110
SQ SEQUENCE 110 AA; 12052 MW; 84E6F2AD219AF95E CRC64;

Query Match 36.7%; Score 483.5; DB 11; Length 110;
Best Local Similarity 83.9%; Pred. No. 2,1e-33;
Matches 94; Conservative 7; Mismatches 8; Indels 3; Gaps 2;

QY 137 PELVPGASVKTICSDSGYAFNSMMNWKORPGGGLMIGRIYGGDSNYNGKFEKKA 196
DB 1 PELVPGASVKTICSDSGYAFNSMMNWKORPGGGLMIGRIYGGDSNYNGKFEKKA 60
QY 197 IITADKSSSTAYMQLSILTSVDSAVYFCARSGL-LRYANDYWGQSTVTS 247
DB 61 TITADKSSSTAYMQLSILTSVDSAVYFCARSGL-LRYANDYWGQSTVTS 110

RESULT 5
Q91WS9 PRELIMINARY; PRT; 233 AA.
AC Q91WS9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strauberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013496; AAH13496.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PR00047; Ig_2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KM Hypothetical protein.
FT NON_TER 1
FT 233 233
SQ SEQUENCE 233 AA; 25781 MW; B1C184DA149A16EB CRC64;

Query Match 36.5%; Score 480.5; DB 11; Length 233;
Best Local Similarity 48.9%; Pred. No. 9,8e-33;
Matches 109; Conservative 11; Mismatches 52; Indels 51; Gaps 4;

QY 1 DIQMTTSSLSASLDRTVSCRASQDRIYNTLWYQKFPDGTVFLIYTSRLQPGVPS 60
DB 20 DIQMTTSSLSASLDRTVSCRASQDRIYNTLWYQKFPDGTVFLIYTSRLQPGVPS 79

QY 61 RFGSGSGTDYELTINLEQEDIGYFCQGNTPPMTFGGKLEIKRGGGSGDGGSGSG 120
DB 80 RFGSGSGTDYELTINLEQEDIGYFCQGNTPPMTFGGKLEIKRGGGSGDGGSGSG 127
QY 121 GSGSGSGSEVQLQSGPELVKPGASVKISCKDSGYAFNSMMNWKORPGGGLMIGRIY 180
DB 128 --ADAAPVSIPEPSSSEQLTSGASV-----VCELANFY 159
QY 181 PG-----DDSNYNGKFEKKAITADKSSSTAYMQLSILT 215
DB 160 PADIYWKIKIDSGERONGVLS--WTDDSDKSTYSMSSTILT 199

RESULT 6
Q9R3H6 PRELIMINARY; PRT; 474 AA.
AC Q9R3H6;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN AU044919.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strauberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025447; AAH25447.1; -.
DR MGD; MG12144667; AU044919.
DR GO; GO:0005489; Electon transporter activity; IEA.
DR GO; GO:0006118; Electon transporter; IEA.
DR InterPro; IPR00345; CytC heme_BS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00190; CYTOCHROME_C; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
KM Hypothetical protein.
SQ SEQUENCE 474 AA; 51748 MW; 8608B57C6CD2874A CRC64;

Query Match 36.3%; Score 478; DB 11; Length 474;
Best Local Similarity 74.0%; Pred. No. 3,9e-32;
Matches 91; Conservative 14; Mismatches 18; Indels 0; Gaps 0;

QY 125 GGSSEVQLQSGPELVKPGASVKISCKDSGYAFNSMMNWKORPGGGLMIGRIYFGDG 184
DB 16 GHSQVQLDSSGPELVKPGASVKISCRASGYAPSSKMMNWKRRPKGGLMIGRIYFGDG 75
QY 185 DSNYNGKFEKKAITADKSSSTAYMQLSILTSVDSAVYFCARSGLLRYANDYWGQSTV 244
DB 76 DTHYSGKFGKAKLTADKSSSTAYMQLSILTSVDSAVYFCARSDYGDYFDWGQATVT 135
QY 245 VSS 247
DB 136 VSS 138

RESULT 7
Q924Q1 PRELIMINARY; PRT; 142 AA.
AC Q924Q1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE V23-D-J-C mu protein (Fragment).
GN V23-D-J-C MU

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RA Kozono Y., Kozono H., Azuma T.,
 RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
 Affinity Maturation of B Cell Antigen Receptors in Response to (4-
 RT Hydroxy-3-Nitrophenyl)Acetyl (NP)."
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB069913; BAB63929.1; -
 DR PIR; F33932; F33932.
 DR PIR; F28833; F28833.
 DR PIR; PH156; PH156.
 DR PIR; PH158; PH158.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 142 AA; 15622 MW; 24A265CE4EA4318B CRC64;

Query Match 35.8%; Score 471; DB 11; Length 142;
 Best Local Similarity 77.3%; Pred. No. 3.3e-32;
 Matches 92; Conservative 7; Mismatches 18; Indels 2; Gaps 1;
 Oy 129 EVQLQDSGPELVKPGASVKISCKDQSGYAFNNSMMNWKQPPGGLGWIGRIYDGDSDNY 188
 Db 1 QVQLQQPGELVKGASVKISCKASGYTFSTYMMHWKQPPGGLGWIGINISNGNTNY 60
 Oy 189 NGKPEKAITLADKSSSTAVYQLSLTSVDSAVYFCARSGILRYANDYMGQSTVSS 247
 Db 61 NEKPKATLTLDKSSSTAVYQLSLTSVDSAVYFCARSGILRYANDYMGQSTVSS 117

RESULT 8
 ID Q91WT1 PRELIMINARY; PRT; 481 AA.
 AC Q91WT1;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DS Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Tissue=Colon;
 RA Strubeberg R.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC013490; AAH13490.1; -
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG_LIKE; 4.
 DR PROSITE; PSS0290; IG_MHC; 2.
 KW Hypothetical protein.
 SQ SEQUENCE 481 AA; 52105 MW; 97DF68D159463F65 CRC64;

Query Match 35.7%; Score 470; DB 11; Length 481;
 Best Local Similarity 73.0%; Pred. No. 1.9e-31;
 Matches 92; Conservative 11; Mismatches 21; Indels 2; Gaps 1;
 Oy 122 GSGGGSGEVQLQDSGPELVKPGASVKISCKDQSGYAFNNSMMNWKQPPGGLGWIGRIY 181
 Db 1 QVQLQQPGELVKGASVKISCKASGYTFSTYMMHWKQPPGGLGWIGINISNGNTNY 60

Db 13 GTAGVQCQVQLDQSGPELVKPGASVKISCKASGYTFSTYIHVWKQPPGGLWIGIY 72
 Oy 182 GGGSSNNGKREGKAITLADKSSSTAVYQLSLTSVDSAVYFCARSGILRYANDYMGQST 241
 Db 73 GGGNTKNEKPKATLTLDKSSSTAVYQLSLTSVDSAVYFCARSGILRYANDYMGQST 130

Query 242 SVTVSS 247
 Db 131 TLTVSS 136

RESULT 9
 ID Q924Q6 PRELIMINARY; PRT; 145 AA.
 AC Q924Q6;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE VH186.2-D-U-C mu protein (fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RA Kozono Y., Kozono H., Azuma T.,
 RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
 Affinity Maturation of B Cell Antigen Receptors in Response to (4-
 RT Hydroxy-3-Nitrophenyl)Acetyl (NP)."
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB067794; BAB63279.1; -
 DR PIR; F28833; F28833.
 DR PIR; F33932; F33932.
 DR PIR; PH105; PH105.
 DR PIR; PH108; PH108.
 DR PIR; PH114; PH114.
 DR PIR; PH118; PH118.
 DR PIR; PH119; PH119.
 DR PIR; PH125; PH125.
 DR PIR; PH126; PH126.
 DR PIR; PH128; PH128.
 DR PIR; PH129; PH129.
 DR PIR; PH131; PH131.
 DR PIR; PH134; PH134.
 DR PIR; PH137; PH137.
 DR PIR; PH139; PH139.
 DR PIR; PH142; PH142.
 DR PIR; PH144; PH144.
 DR PIR; PH147; PH147.
 DR PIR; PH149; PH149.
 DR PIR; PH150; PH150.
 DR PIR; PH151; PH151.
 DR PIR; PH152; PH152.
 DR PIR; PH153; PH153.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 145 AA; 16011 MW; 9BC0846D40DF972A CRC64;

Query Match 35.6%; Score 469.5; DB 11; Length 145;
 Best Local Similarity 76.7%; Pred. No. 4.6e-32;
 Matches 92; Conservative 7; Mismatches 20; Indels 1; Gaps 1;

Oy 129 EVQLQDSGPELVKPGASVKISCKDQSGYAFNNSMMNWKQPPGGLGWIGRIYDGDSDNY 188
 Db 1 QVQLQQPGELVKGASVKISCKASGYTFSTYMMHWKQPPGGLGWIGIDPNSGGTKY 60
 Oy 189 NGKPEKAITLADKSSSTAVYQLSLTSVDSAVYFCARSGILRYANDYMGQSTVSS 247

Db 61 NEKFKSKATLTVDKPSSTAYMQLSSITSDSAVYCAASTLSHYAMDMYGGTSTVSS 120

RESULT 10

Q92409 PRELIMINARY; PRT; 145 AA.

AC Q92409
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
 DE VH186.2-D-J-C mu protein (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCB1_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=CS7BL/6;
 RA Kozono Y., Kozono H., Azuma T.;
 RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
 Affinity Maturation of B Cell Antigen Receptors in Response to (4-
 Hydroxy-3-Nitrophenyl)Acetyl (NP)."
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB067791; BAB63276.1; -

DR PIR; F28833; F28833.
 DR PIR; F33932; F33932.
 DR PIR; PH105; PH105.
 DR PIR; PH108; PH108.
 DR PIR; PH114; PH114.
 DR PIR; PH118; PH118.
 DR PIR; PH119; PH119.
 DR PIR; PH125; PH125.
 DR PIR; PH126; PH126.
 DR PIR; PH128; PH128.
 DR PIR; PH129; PH129.
 DR PIR; PH131; PH131.
 DR PIR; PH134; PH134.
 DR PIR; PH137; PH137.
 DR PIR; PH139; PH139.
 DR PIR; PH142; PH142.
 DR PIR; PH144; PH144.
 DR PIR; PH147; PH147.
 DR PIR; PH149; PH149.
 DR PIR; PH150; PH150.
 DR PIR; PH151; PH151.
 DR PIR; PH152; PH152.
 DR PIR; PH153; PH153.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SMO0406; IgV_1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 FT NON_TER 1
 FT 145
 SQ SEQUENCE 145 AA; 16001 MW; 0F409E809F333D2 CRC64;

Query Match 35.3%; Score 465.5; DB 11; Length 145;
 Best Local Similarity 75.8%; Pred. No. 1e-31;
 Matches 91; Conservative 8; Mismatches 20; Indels 1; Gaps 1;

QY 129 EVOLQSGPELVKPGASVKISCKDGGYAFNSSMMWVKORPGQGLEMTGIRITPGGDSNY 188
 Db 1 QVQLQPGAEIVKPGASVKISCKASGYTFTSYMMHWVKORFGKGLIEWIGRIDPNSGGTKY 60

QY 189 NGKFEKAILITADKSSSTAYMQLSSITSDSAVYFCARGLAR-YAMDYGGTSTVSS 247
 Db 61 NEKFKSKATLTVDKPSSTAYMQLSSITSDSAVYCARGLITTYAMDMYGGTSTVSS 120

RESULT 11

Q924R1 PRELIMINARY; PRT; 145 AA.

AC Q924R1
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
 DE VH186.2-D-J-C mu protein (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCB1_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=CS7BL/6;
 RA Kozono Y., Kozono H., Azuma T.;
 RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
 Affinity Maturation of B Cell Antigen Receptors in Response to (4-
 Hydroxy-3-Nitrophenyl)Acetyl (NP)."
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB067789; BAB63274.1; -

DR PIR; F28833; F28833.
 DR PIR; F33932; F33932.
 DR PIR; PH105; PH105.
 DR PIR; PH108; PH108.
 DR PIR; PH114; PH114.
 DR PIR; PH118; PH118.
 DR PIR; PH119; PH119.
 DR PIR; PH125; PH125.
 DR PIR; PH126; PH126.
 DR PIR; PH128; PH128.
 DR PIR; PH129; PH129.
 DR PIR; PH131; PH131.
 DR PIR; PH134; PH134.
 DR PIR; PH137; PH137.
 DR PIR; PH139; PH139.
 DR PIR; PH142; PH142.
 DR PIR; PH144; PH144.
 DR PIR; PH147; PH147.
 DR PIR; PH149; PH149.
 DR PIR; PH150; PH150.
 DR PIR; PH151; PH151.
 DR PIR; PH152; PH152.
 DR PIR; PH153; PH153.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SMO0406; IgV_1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 FT NON_TER 1
 FT 145
 SQ SEQUENCE 145 AA; 15979 MW; 0162D0A26C746C04 CRC64;

Query Match 35.3%; Score 464.5; DB 11; Length 145;
 Best Local Similarity 75.8%; Pred. No. 1.2e-31;
 Matches 91; Conservative 7; Mismatches 21; Indels 1; Gaps 1;

QY 129 EVOLQSGPELVKPGASVKISCKDGGYAFNSSMMWVKORPGQGLEMTGIRITPGGDSNY 188
 Db 1 QVQLQPGAEIVKPGASVKISCKASGYTFTSYMMHWVKORFGKGLIEWIGRIDPNSGGTKY 60

QY 189 NGKFEKAILITADKSSSTAYMQLSSITSDSAVYFCAR-SGLRYAMDYGGTSTVSS 247
 Db 61 NEKFKSKATLTVDKPSSTAYMQLSSITSDSAVYCARYGSSFYAMDMYGGTSTVSS 120

RESULT 12

Q924R4 PRELIMINARY; PRT; 145 AA.

AC Q924R4
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
 DE VH186.2-D-J-C mu protein (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=C57BL/6j
RA	Kozono Y., Kozono H., Azuma T.;
RT	"Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT	Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT	Hydroxy-3-Nitrophenyl)Acetyl (NP)."
RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AB067785; BAB63270.1; -
DR	PIR; F28833; F28833.
DR	PIR; F33932; F33932.
DR	PIR; PH1105; PH1105.
DR	PIR; PH1108; PH1108.
DR	PIR; PH1114; PH1114.
DR	PIR; PH1118; PH1118.
DR	PIR; PH1119; PH1119.
DR	PIR; PH1125; PH1125.
DR	PIR; PH1126; PH1126.
DR	PIR; PH1128; PH1128.
DR	PIR; PH1129; PH1129.
DR	PIR; PH1131; PH1131.
DR	PIR; PH1134; PH1134.
DR	PIR; PH1137; PH1137.
DR	PIR; PH1139; PH1139.
DR	PIR; PH1142; PH1142.
DR	PIR; PH1144; PH1144.
DR	PIR; PH1147; PH1147.
DR	PIR; PH1149; PH1149.
DR	PIR; PH1150; PH1150.
DR	PIR; PH1151; PH1151.
DR	PIR; PH1152; PH1152.
DR	PIR; PH1153; PH1153.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003596; Ig_V.
DR	Pfam; PF00047; Ig; 1.
DR	SMART; SM00406; IgV; 1.
DR	PROSITE; PS50835; IG_LIKE; 1.
FT	NON TER 1
FT	NON TER 1
SQ	SEQUENCE 145 AA; 145 RESIDUES; ECDBIA13F05B8AA CXC64;
Query Match	35.3%; Score 464.5; DB 11; Length 145;
Best Local Similarity	75.8%; Pred.No.1.2e-31;
Matches 91; Conservative 7; Mismatches 21; Indels 1; Gaps 1	
OY	129 EVOLQGSGPLVYPGASVKISCKDSCGFANSEMMNMWVKKPFGQGLEWIGRIYEDDGDSNY 188
DB	1 QVQLQQGAGLVLPFGASVYLKSCASGYTTSYIMHWYQRGRGLMIIGRIDPSGGTKY 60
OY	189 NGKEFGKAIIITADKSSSTAWMQLSLTVSDSAVFCAESGE-LRYAMDYWGQGSTVTVS 247
DB	61 NEKFKSATLTVDKPSTAFWMLSLTSEDASAVYCCASDYDDYAMDYGCGSTVTVS 120
RESULT 13	
ID	Q9ZIC4 PRELIMINARY; PRT; 118 AA.
AC	Q9ZIC4;
DT	01-MAY-1999 (TREMBLrel. 10, Created)
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT	01-OCT-2003 (TREMBLrel. 25, last annotation update)
DE	Anti-porcine VCM mAb 3f4 heavy chain variable region (fragment).
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=Balb/c;
RA	Meslier J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
RA	Matlis L.W., Evans W.J.;

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RT "Humanized porcine VCAH-specific monoclonal antibodies with chimeric
RT IgG2/G4 constant regions block human leukocyte binding to porcine
RT endothelial cells."
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL/ U78801; AAD00293.1; -.
DR HSSP; P01810; 2FBF.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003586; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT TER 118
SQ SEQUENCE 118 AA; 13036 MW; 90EEC559D31EC4FC CRC64;

Query Match 35.2%; Score 463.5; DB 11; Length 118;
Best Local Similarity 74.8%; Pred. No. 1.1e-31;
Matches 89; Conservative 10; Mismatches 19; Indels 1; Gaps 1

QY 129 EYVQGGSGELVKPSPASYKISCKDGYAFNSMWNWTKQSPGGGLTWIGRIYGGDSNY 188
Db 1 QVQVQGGSELKRPASVKLSCKASGYRNSYNWQWKQPPGGGLEWIGALYGGDSIT 60

QY 189 NGKFEKALITLADKSSSTAYNQLSLTSVDSAVVFCARSGILRYANDYWGQSTVTSS 247
Db 61 TQFRRKATLTADKSSSTAYNQLSLTSVDSAVVFCARRIVGV-PDYWGQGLTTLVSS 118

RESULT 14
QSR062 PRELIMINARY; PR3; 234 AA.
AC QSR062;
DT 01-JUN-2002 (T-EMBLrel. 21, Created)
DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId:10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC027418; AAH27418.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003586; IG_v.
DR Pfam; PF00047; IG_2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
DR Hypothetical protein.
SQ SEQUENCE 234 AA; 25857 MW; 4EB08C81426A8A1 CRC64;

Query Match 35.1%; Score 462.5; DB 11; Length 234;
Best Local Similarity 48.0%; Pred. No. 3.3e-31;
Matches 107; Conservative 13; Mismatches 52; Indels 51; Gaps 4

QY 1 DIOMTOTSLSASLGDRVTVSCRASQDIRYLNWYQOKPDGTVKFLIYYTSLQGVPS 60
Db 21 DIOMTOTSLSASLGDRVTVSCASQDIRYLNWYQOKPDGTVKFLIYYTSLHGVPS 80

QY 61 RFGSGSGTDYVLTNNLEQEDIGTFPCQGGNTPEMTFGGTFKLEIRGGGSGDGGSGG 120
Db 81 RFGSGSGTHYVLTNNLEPEDIAIYYVCOQYSCFPFFGSGTKLEIRK----- 128

QY 121 GGGGGGGSEVQLQGSGPELVKPGASVKISCDSDYAFANSSMWNWYQRPQGLWETGR 180
Db 129 --ADAAPTVITPPSSBQITSGASV-----VCFINPFY 160

QY 181 PG-----DGDSDNYNGKFEKALITLADKSSSTAYNQLSLT 215

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Db 161 PKDINVKRKIDGSEKQNGVLNS--WTDDSKDSTYSMSSTLT 200

RESULT 15

092403 PRELIMINARY; PRT; 146 AA.
ID 092403
AC 092403;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE VHL86.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y, Kozono H, Azuma T;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP)."
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067797; BAB63282.1; -
DR PIR; F28833; F28833.
DR PIR; F33932; F33932.
DR PIR; PH1105; PH1105.
DR PIR; PH1108; PH1108.
DR PIR; PH1114; PH1114.
DR PIR; PH1118; PH1118.
DR PIR; PH1119; PH1119.
DR PIR; PH1125; PH1125.
DR PIR; PH1126; PH1126.
DR PIR; PH1128; PH1128.
DR PIR; PH1129; PH1129.
DR PIR; PH1131; PH1131.
DR PIR; PH1134; PH1134.
DR PIR; PH1137; PH1137.
DR PIR; PH1139; PH1139.
DR PIR; PH1142; PH1142.
DR PIR; PH1144; PH1144.
DR PIR; PH1147; PH1147.
DR PIR; PH1149; PH1149.
DR PIR; PH1150; PH1150.
DR PIR; PH1151; PH1151.
DR PIR; PH1152; PH1152.
DR PIR; PH1153; PH1153.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV_1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 146 AA; 146 CAA8DD6B1955807F CRC64;

Query Match 35.0%; Score 461; DB 11; Length 146;
Best Local Similarity 75.2%; Pred. No. 2.4e-31;
Matches 91; Conservative 7; Mismatches 21; Indels 2; Gaps 1;

QY 129 EVOLQSGPELVKPGASVKISCKDQGYAFNNSMHWYKORPGQGLEWIGRIYPGDSDNY 188

Db 1 QVQLQDQPGAEIVKCAVYKISCKASGTFITSYMMHWKQRPGRGLEWIGRIDPNSGGTKY 60

QY 189 NGKREGKAITADYSSSTAYWQLSLTSVDSAVTFCAR--GLIRYANDYWGQSTSYTVS 246

Db 61 NEKFKSATLTVDKPSSTAYWQLSLTSSEDAVYTCARSLYDYGVDANDYWGQSTSYTVS 120

QY 247 S 247

Db 121 S 121

Search completed: April 22, 2004, 11:56:32
Job time : 38 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 22, 2004, 11:48:48 ; Search time 10.5 Seconds
(without alignments)
1224.888 Million cell updates/sec

Title: US-10-620-049-23

Perfect score: 1317

Sequence: 1 DIQMTQTSSLSASIGDRVT.....GLRYAMDYWGCGTSVTWSS 247

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	511	38.8	108	1	KV5K_MOUSE
2	510	38.7	108	1	KV5N_MOUSE
3	509	38.6	108	1	KV5L_MOUSE
4	501	38.0	108	1	KV5O_MOUSE
5	497	37.7	108	1	KV5K_MOUSE
6	476	36.1	108	1	KV5U_MOUSE
7	457	34.7	108	1	KV5U_MOUSE
8	443	33.6	140	1	HV02_MOUSE
9	440.5	33.4	139	1	HV07_MOUSE
10	430	32.6	120	1	HV03_MOUSE
11	426.5	32.4	137	1	HV11_MOUSE
12	423	32.1	117	1	HV05_MOUSE
13	421	32.0	117	1	HV06_MOUSE
14	419	31.8	138	1	HV48_MOUSE
15	415	31.5	117	1	HV13_MOUSE
16	414	31.4	121	1	HV01_MOUSE
17	413	31.4	117	1	HV12_MOUSE
18	406.5	30.9	118	1	HV51_MOUSE
19	405	30.8	117	1	HV05_MOUSE
20	403	30.6	117	1	HV04_MOUSE
21	400.5	30.4	120	1	HV50_MOUSE
22	395	30.0	108	1	KV5P_MOUSE
23	394	29.9	108	1	KV1Y_HUMAN
24	392	29.8	130	1	KV5G_MOUSE
25	388	29.5	117	1	HV09_MOUSE
26	386	29.3	108	1	KV10_HUMAN
27	384	29.2	108	1	KV18_HUMAN
28	383	29.1	108	1	KV1A_HUMAN
29	382	29.0	108	1	KV1R_HUMAN
30	381	28.9	108	1	KV1P_HUMAN
31	379	28.8	117	1	HV10_MOUSE
32	377	28.6	117	1	HV14_MOUSE

34	372	28.2	129	1	KV1W_HUMAN	P04431 homo sapien
35	371	28.2	108	1	KV1S_HUMAN	P01611 homo sapien
36	369	28.0	108	1	KV1M_HUMAN	P01605 homo sapien
37	369	28.0	108	1	KV1O_HUMAN	P01609 homo sapien
38	368	27.9	108	1	KV1E_HUMAN	P01597 homo sapien
39	368	27.9	108	1	KV1H_HUMAN	P01600 homo sapien
40	368	27.9	108	1	KV1V_HUMAN	P04430 homo sapien
41	367	27.9	108	1	KV1G_HUMAN	P01599 homo sapien
42	366	27.8	108	1	KV1C_HUMAN	P01595 homo sapien
43	362	27.5	128	1	KV5E_MOUSE	P01637 mus musculu
44	362	27.5	136	1	HV1S_MOUSE	P01759 mus musculu
45	361	27.4	108	1	KV1L_HUMAN	P01604 homo sapien

ALIGNMENTS

RESULT 1	ID	Query Match	Score	Length	DB ID	Description
1	KV5K_MOUSE	38.8%	511	108	1	KV5K_MOUSE
AC	P01644	38.7%	510	108	1	KV5N_MOUSE
DT	21-JUL-1986 (Rel. 01, Created)	38.6%	509	108	1	KV5L_MOUSE
DT	21-JUL-1986 (Rel. 01, Last sequence update)	38.0%	501	108	1	KV5O_MOUSE
DT	28-FEB-2003 (Rel. 41, Last annotation update)	37.7%	497	108	1	KV5K_MOUSE
DE	Ig kappa chain V-V region HP R16.7.	36.1%	476	108	1	KV5U_MOUSE
OS	Mus musculus (Mouse).	34.7%	457	108	1	KV5U_MOUSE
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	33.6%	443	140	1	HV02_MOUSE
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	33.4%	440.5	139	1	HV07_MOUSE
OX	NCBI_TaxID=10090;	32.6%	430	120	1	HV03_MOUSE
RN	[1]	32.4%	426.5	137	1	HV11_MOUSE
RP	SEQUENCE.	32.1%	423	117	1	HV05_MOUSE
RC	STRAIN=A/Y;	32.0%	421	117	1	HV06_MOUSE
RA	MEDLINE=82150934; PubMed=6801658;	31.8%	419	138	1	HV48_MOUSE
RX	Siegalman M., Capra J.D.;	31.5%	415	117	1	HV13_MOUSE
RT	"Complete amino acid sequence of light chain variable regions derived from five monoclonal anti-p-azophenylarsenate antibodies differing	31.4%	414	121	1	HV01_MOUSE
RT	with respect to a crossreactive idiotype."	31.4%	413	117	1	HV12_MOUSE
RL	Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).	30.9%	406.5	118	1	HV51_MOUSE
CC	-I- MISCELLANEOUS: Anti-arsenate hydriodoma protein.	30.8%	405	117	1	HV05_MOUSE
DR	PIR; A01927; KMSAR.	30.6%	403	117	1	HV04_MOUSE
DR	HSSP; P01607; IREI.	30.4%	400.5	120	1	HV50_MOUSE
DR	InterPro; IPR007110; Ig-like.	30.0%	395	108	1	KV5P_MOUSE
DR	InterPro; IPR003596; Ig_V.	29.9%	394	108	1	KV1Y_HUMAN
DR	Pfam; PF00047; Ig; 1.	29.8%	392	130	1	KV5G_MOUSE
DR	SMART; SMO0406; IgV; 1.	29.5%	388	117	1	HV09_MOUSE
DR	PROSITE; PS50835; IG LIKE; 1.	29.3%	386	108	1	KV10_HUMAN
KM	Immunoglobulin V region.	29.2%	384	108	1	KV18_HUMAN
FT	DOMAIN 1 23	29.1%	383	108	1	KV1A_HUMAN
FT	DOMAIN 2 34	29.0%	382	108	1	KV1R_HUMAN
FT	DOMAIN 3 49	28.9%	381	108	1	KV1P_HUMAN
FT	DOMAIN 4 56	28.8%	379	117	1	HV10_MOUSE
FT	DOMAIN 5 78	28.6%	377	117	1	HV14_MOUSE
FT	DOMAIN 6 89					
FT	DOMAIN 7 97					
FT	DOMAIN 8 108					
FT	DISULFID 23					
FT	NON TER 108					
FT	SEQUENCE 108 AA; 11910 MW; A554642C63EFF597 CRC64;					
Query Match	38.8%	Score 511;	DB 1;	Length 108;		
Best Local Similarity	90.7%	Pred. No. 5.4e-33;				
Matches	98;	Conservative 3;	Mismatches 7;	Indels 0;	Gaps 0;	
QY	1	DIQMTQTSSLSASIGDRVTSCRASQDIRNYLWYQKPGTYKFLYYTSRLQPGVPS	60			
DB	1	DIQMTQTSSLSASIGDRVTISCRASQDISNYLWYQKPGTYKFLYYTSRLHSGVPS	60			
QY	61	RFGSGSGSDYSLTINNEQEDIGTFPCQGNTPPMTFGGTXLEIKR	108			
DB	61	RFGSGSGSDYSLTINNEQEDIGTFPCQGNTPPMTFGGTXLEIKR	108			
RESULT 2						
KV5N_MOUSE						

ID KVEN MOUSE STANDARD; PRT; 108 AA.
 AC P01647;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ig kappa chain V-V region HP 124E1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RX STRAIN=A/J;
 RC MEDLINE=82150934; PubMed=6801658;
 RA Siegelman M., Capra J.D.;
 RT "Complete amino acid sequence of light chain variable regions derived
 from five monoclonal anti-p-azophenylarsenate antibodies differing
 with respect to a crossreactive idiotype.";
 RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
 CC -1- MISCELLANEOUS: Anti-arsenate hydridoma protein.
 DR HSP; P01607; IREI.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 3 49 FRAMEWORK-2.
 FT DOMAIN 4 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 5 57 FRAMEWORK-3.
 FT DOMAIN 6 97 FRAMEWORK-4.
 FT DISULFID 98 108 BY SIMILARITY.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11965 MW; 39971BC653EF6A2 CRC64;
 Query Match 38.7%; Score 510; DB 1; Length 108;
 Best Local Similarity 90.7%; Pred. No. 6.5e-33;
 Matches 98; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
 QY 1 DIOMTQTSSLSASISGDRVTWSCRASODIRNYLMWYQOKPDGTGKFLIYTSRLQPGVPS 60
 DB 1 DIOMTQTSSLSASISGDRVTWSCRASODIRNYLMWYQOKPDGTGKFLIYTSRLHSGVPS 60
 QY 61 RPSGSGSGTDTYSLTINNEQEDIGYFCQCGNTPEPTFGGKLEIKR 108
 DB 61 RPSGSGSGTDTYSLTINNEQEDIGYFCQCGNTPEPTFGGKLEIKR 108
 DB 61 RPSGSGSGTDTYSLTINNEQEDIGYFCQCGNTPEPTFGGKLEIKR 108
 RESULT 3
 KVEN MOUSE STANDARD; PRT; 108 AA.
 AC P01645;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ig kappa chain V-V region HP 93G7.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RX STRAIN=A/J;
 RC MEDLINE=82150934; PubMed=6801658;
 RA Siegelman M., Capra J.D.;
 RT "Complete amino acid sequence of light chain variable regions derived
 from five monoclonal anti-p-azophenylarsenate antibodies differing
 with respect to a crossreactive idiotype.";
 RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
 CC -1- MISCELLANEOUS: Anti-arsenate hydridoma protein.
 DR HSP; P01607; IREI.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 3 49 FRAMEWORK-2.
 FT DOMAIN 4 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 5 57 FRAMEWORK-3.
 FT DOMAIN 6 97 FRAMEWORK-4.
 FT DISULFID 98 108 BY SIMILARITY.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11961 MW; D52BDA5E9A45291C CRC64;
 Query Match 38.0%; Score 501; DB 1; Length 108;

DR HSP; P01607; IREI.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 3 49 FRAMEWORK-2.
 FT DOMAIN 4 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 5 57 FRAMEWORK-3.
 FT DOMAIN 6 97 FRAMEWORK-4.
 FT DISULFID 98 108 BY SIMILARITY.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11954 MW; 22F4642C63EF658E CRC64;
 Query Match 38.6%; Score 509; DB 1; Length 108;
 Best Local Similarity 90.7%; Pred. No. 7.7e-33;
 Matches 98; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
 QY 1 DIOMTQTSSLSASISGDRVTWSCRASODIRNYLMWYQOKPDGTGKFLIYTSRLQPGVPS 60
 DB 1 DIOMTQTSSLSASISGDRVTWSCRASODIRNYLMWYQOKPDGTGKFLIYTSRLHSGVPS 60
 QY 61 RPSGSGSGTDTYSLTINNEQEDIGYFCQCGNTPEPTFGGKLEIKR 108
 DB 61 RPSGSGSGTDTYSLTINNEQEDIGYFCQCGNTPEPTFGGKLEIKR 108
 DB 61 RPSGSGSGTDTYSLTINNEQEDIGYFCQCGNTPEPTFGGKLEIKR 108
 RESULT 4
 KVEN MOUSE STANDARD; PRT; 108 AA.
 AC P01648;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ig kappa chain V-V region HP 91A3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RX STRAIN=A/J;
 RC MEDLINE=82150934; PubMed=6801658;
 RA Siegelman M., Capra J.D.;
 RT "Complete amino acid sequence of light chain variable regions derived
 from five monoclonal anti-p-azophenylarsenate antibodies differing
 with respect to a crossreactive idiotype.";
 RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
 CC -1- MISCELLANEOUS: Anti-arsenate hydridoma protein.
 DR HSP; P01607; IREI.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 3 49 FRAMEWORK-2.
 FT DOMAIN 4 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 5 57 FRAMEWORK-3.
 FT DOMAIN 6 97 FRAMEWORK-4.
 FT DISULFID 98 108 BY SIMILARITY.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11961 MW; D52BDA5E9A45291C CRC64;
 Query Match 38.0%; Score 501; DB 1; Length 108;

Matches 96; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQMTQTSSISASLGDRVTWSCASODIRNYLNMWYQKPGDGYKFLIYTSRLQGVPS 60
 DB 1 DIQMTQTSSISASLGDRVTWSCASODIRNYLNMWYQKPGDGYKFLIYTSRLHSGVPS 60
 QY 61 RFSGSGSGTDYSLTINNLEQEDIGTYFCQCGNTPTWTFGGGTKEIKR 108
 DB 61 RFSGSGSGTDYSLTINNLEQEDISTYFCQCGNALPRTFGGKTLEIKR 108

RESULT 5

KV5M_MOUSE STANDARD; PRT; 108 AA.
 AC P01646;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ig kappa chain V-V region HP 12356.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_Taxid=10090;
 RN [1]

RA SIEGELMAN M., Capra J.D.;
 RT "Complete amino acid sequence of light chain variable regions derived from five monoclonal anti-P-azophenylarsenate antibodies differing with respect to a crossreactive idiotype."
 RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
 CC -1- MISCELLANEOUS: Anti-arsenate hybridoma protein.
 DR HSP, P01607, IREI.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IgV; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.

DR Immunoglobulin V region.
 KW DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 1 23 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 24 34 FRAMEWORK-2.
 FT DOMAIN 35 49 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 50 56 FRAMEWORK-3.
 FT DOMAIN 57 88 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 89 97 FRAMEWORK-4.
 FT DOMAIN 98 108 BY SIMILARITY.
 FT DISULFID 23 88
 FT NON_TER 108
 SQ SEQUENCE 108 AA; 11989 MW; 4C98599C08BA09A CRC64;

Query Match 37.7%; Score 497; DB 1; Length 108;
 Best Local Similarity 88.9%; Pred. No. 6, Se-33;
 Matches 96; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQMTQTSSISASLGDRVTWSCASODIRNYLNMWYQKPGDGYKFLIYTSRLQGVPS 60
 DB 1 DIQMTQTSSISASLGDRVTWSCASODIRNYLNMWYQKPGDGYKFLIYTSRLHSGVPS 60
 QY 61 RFSGSGSGTDYSLTINNLEQEDIGTYFCQCGNTPTWTFGGGTKEIKR 108
 DB 61 RFSGSGSGTDYSLTINNLEQEDISTYFCQCGNALPRTFGGKTLEIKR 108

RESULT 6

KV5U_MOUSE STANDARD; PRT; 108 AA.
 AC P04946;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-V region NOS-89.4.
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83271467; PubMed=6877353;
 RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
 RT "RNA sequences define an unusually restricted IgG response to 2-phenylloxazalone and its early diversification."
 RL Nature 304:320-324(1983).
 CC -1- MISCELLANEOUS: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
 CC -----
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 CC -----

CC EMBL; K00745; AAA38690.1; -.
 DR HSP, P01607, IREI.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; IgV; 1.
 DR SMART: SM00406; IgV; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Hybridoma.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 98 107 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON_TER 108
 SQ SEQUENCE 108 AA; 11866 MW; DB2C885920DC6DD CRC64;

Query Match 36.1%; Score 476; DB 1; Length 108;
 Best Local Similarity 84.3%; Pred. No. 2, Se-30;
 Matches 91; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIQMTQTSSISASLGDRVTWSCASODIRNYLNMWYQKPGDGYKFLIYTSRLQGVPS 60
 DB 1 DIQMTQTSSISASLGDRVTWSCASODIRNYLNMWYQKPGDGYKFLIYTSRLHSGVPS 60
 QY 61 RFSGSGSGTDYSLTINNLEQEDIGTYFCQCGNTPTWTFGGGTKEIKR 108
 DB 61 RFSGSGSGTDYSLTINNLEQEDISTYFCQCGNTPTWTFGGGTKEIKR 108

RESULT 7

KV5U_MOUSE STANDARD; PRT; 108 AA.
 AC P01643;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-V region MOPC 173.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=76091934; PubMed=812636;
 RA Schiff C., Fougereau M.;
 RT "Determination of the primary structure of a mouse IgG2a immunoglobulin. Amino-acid sequence of the light chain."
 RL Eur. J. Biochem. 59:525-537(1975).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
 DR PIR, A01926; KMG573.

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DR HSPB, P01607; 1REI.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; 1g; 1.
DR SMART; SM00406; 1g; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR Immunoglobulin V region.
KM
FT DOMAIN 1 23
FT 24 34 FRAMEWORK-1.
FT 35 49 FRAMEWORK-2.
FT 50 56 COMPLEMENTARITY-DETERMINING-2.
FT 57 88 FRAMEWORK-3.
FT 89 97 COMPLEMENTARITY-DETERMINING-3.
FT 98 108 FRAMEWORK-4.
FT 109 108 BY SIMILARITY.
FT DISULFID 23 88
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11819 MW; 2AD29D2A72A0A3 CRC64;

Query Match
Best Local Similarity 34.7%; Score 457; DB 1; Length 108;
Matches 86; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIQNTQTSSLSASLGPRVYSCASODIRNYLAWYQKPDGYKFLITYTSKLGQVPS 60
DB 1 DIQNTQTSSLSASLGPRVYSCASODIRNYLAWYQKPDGYKFLITYTSKLGQVPS 60

QY 61 RFSGSGSGTGYSLTINNLECEDEICTGYFCQOQNPPTWFGGTGKLEIKR 108
DB 61 RFSGSGSGTGYSLTINNLECEDEICTGYFCQOQNPPTWFGGTGKLEIKR 108

RESULT 8
HVO2_MOUSE STANDARD; PRT; 140 AA.
ID HVO2_MOUSE
AC P01746;
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 1g heavy chain V region 9367 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A/J;
RX MEDLINE=82152818; PubMed=6801765;
RA Sline U.; Rablites T.H.; Estees P.; Slaughter C.; Tucker P.W.;
RA Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain."
RL Science 246:309-311(1982).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC
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CC
CC EMBL; J00493; AAA8128.1; -.
CC PIR; A94264; HVMSG7.
CC HSPB; P01610; 2PRF.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; 1g; 1.
DR SMART; SM00406; 1g; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR Immunoglobulin V region; Hybridoma; signal.
FT SIGNAL 1 19
FT CHAIN 20 140 IG HEAVY CHAIN V REGION 9367.

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FT DOMAIN 20 139 IG-LIKE.
FT NON TER 140 140
SQ SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5C88 CRC64;

Query Match
Best Local Similarity 33.6%; Score 443; DB 1; Length 140;
Matches 90; Conservative 8; Mismatches 27; Indels 2; Gaps 1;

QY 123 SGGGSESEVQLQSSGPGLYKPCASVKISCKDGYAFNSMNMWYQKPGQGLEMTGRITYP 182
DB 14 TAGHSEVQLQSSGAEVLRAGSSVMSCKSGYFTSYGINWVRQPGGLEMTGYNIPG 73

QY 183 DGDSSNYGKFEFGKAILLTADKSSSTAYMQLSLSVDSAVYFCARSGLL--RYAMDYWGQG 240
DB 74 NGYINYNKRFKPKNTLTVDKSSSTAYMQLRSLTSDSAVYFCARSHYGGSDYDFDYGQG 133

QY 241 TSVYTS 247
DB 134 TPLTVSS 140

RESULT 9
HVO7_MOUSE STANDARD; PRT; 139 AA.
ID HVO7_MOUSE
AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 1g heavy chain V region B1-8/186-2 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Botwell A.L.M.; Parkind M.; Reith M.; Tanishi Kari T.; Rajewsky K.;
RA Baltimore D.;
RT "Heavy chain variable region contribution to the Npb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region."
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC
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CC
CC EMBL; J00529; AAA81170.1; -.
CC PIR; A90809; MEMS18.
CC PDB; 1AEU; 27-MAY-98.
DR PDB; 1AEU; 15-JUL-98.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; 1g; 1.
DR SMART; SM00406; 1g; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR Immunoglobulin V region; signal; 3D-structure.
FT SIGNAL 1 19
FT CHAIN 20 139 IG HEAVY CHAIN V REGION B1-8/186-2.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 124 D SEGMENT.
FT DOMAIN 125 139 JH2 SEGMENT.

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PT DISULFID 41 115 BY SIMILARITY.
FT NON TER 139 139
SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FD0C9F465 CRC64;

Query Match
Best Local Similarity 33.4%; Score 440.5; DB 1; Length 139;
Matches 87; Conservative 10; Mismatches 26; Indels 1; Gaps 1;

QY 135 GGGSEVQLQSGPELVKPGASVKISCKDGYAFNNSMMNWKQRPQGGLWIGRIYPDG 184
DB 16 GVHSGVQLQPGAEIVKPGASVKISCKASGYTFSTYMMHWKQRPGRGLEWIGRIDPNSG 75
QY 185 DSNYNGKFEKALITLADKSSSTAYNQSLTSVDSAVYFCARSGILRYA-MDYMGQGTSTV 243
DB 76 GTRKNEKFSKATLTIDKPSSTAYNQSLTSVDSAVYFCARSDYVYSSYFDYMGQGTTL 135
QY 244 TVSS 247
DB 136 TVSS 139

RESULT 10
ID HV03_MOUSE STANDARD; PRT; 120 AA.
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V region 36-65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RP SEQUENCE FROM N.A.
RX MEDLINE=83131846; PubMed=6186498;
RA Stekevitz M., Gelfer M.L., Brodeur P., Riblet R.,
RA Marshak-Rothstein A.;
RT "The genetic basis of antibody production: the dominant anti-arsenate
RT idotype response of the strain A mouse.";
RL Eur. J. Immunol. 12:1023-1032(1982).
CC -1- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC SEGMENT, JH2.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSSP; P01789; IMCP.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT DOMAIN 1 111
FT NON TER 120
SQ SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;

Query Match
Best Local Similarity 32.6%; Score 430; DB 1; Length 120;
Matches 86; Conservative 9; Mismatches 23; Indels 2; Gaps 1;

QY 130 VOIQSGPELVKPGASVKISCKDGYAFNNSMMNWKQRPQGGLWIGRIYPDGDSNTN 189
DB 1 VOIQSGAEIVKPGASVKISCKASGYTFSTYMMHWKQRPGRGLEWIGRIYPDGNTN 60
QY 190 GTRKNEKFSKATLTIDKSSSTAYNQSLTSVDSAVYFCARSGIL--RYANDYMGQGTSTVSS 247
DB 61 EKTRGKTLTVDSSTAYNQSLTSVDSAVYFCARSDYVYSSYFDYMGQGTTLTVSS 120

RESULT 11
ID HV11_MOUSE STANDARD; PRT; 137 AA.

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AC P01755;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG heavy chain V region 543 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Bochwail A.L.M., Paskind M., Rech M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NpB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
DE Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THE GAMMA-2A CHAIN WEA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00539; AAA38172.1; -.
DR PIR; A02038; GZMS43.
DR HSSP; P01810; 2FBU.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KM Immunoglobulin V region; Signal.
FT CHAIN 1 19
FT SIGNAL 1 19
FT CHAIN 20 137
FT DOMAIN 20 49
FT DOMAIN 50 54
FT DOMAIN 55 68
FT DOMAIN 69 85
FT DOMAIN 86 117
FT DOMAIN 118 122
FT DOMAIN 123 137
FT DISULFID 41 115
FT NON TER 137
SQ SEQUENCE 137 AA; 15200 MW; ADD5881BF448BEC9 CRC64;

Query Match
Best Local Similarity 32.4%; Score 426.5; DB 1; Length 137;
Matches 86; Conservative 8; Mismatches 28; Indels 1; Gaps 1;

QY 125 GGGSEVQLQSGPELVKPGASVKISCKDGYAFNNSMMNWKQRPQGGLWIGRIYPDG 184
DB 16 GVHSGVQLQPGAEIVKPGASVKISCKASGYTFSTYMMHWKQRPGRGLEWIGRIDPNSG 75
QY 185 DSNYNGKFEKALITLADKSSSTAYNQSLTSVDSAVYFCARSGILRYANDYMGQGTSTV 244
DB 76 GTRKNEKFSKATLTIDKPSSTAYNQSLTSVDSAVYFCARSDYVYSSYFDYMGQGTTLT 134
QY 245 VSS 247
DB 135 VSS 137

RESULT 12
ID HV52_MOUSE STANDARD; PRT; 117 AA.
AC P06327;
DT 01-JAN-1988 (Rel. 06, Created)

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DT 01-JUN-1988 (Rel. 06, last sequence update)
 DT 15-JUL-1999 (Rel. 38, last annotation update)
 DE IG heavy chain V region VH58 A1/A4 precursor.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 RN [1]
 RE SEQUENCE FROM N.A.
 RX MEDLINE=8509340; PubMed=2578321;
 RA Yancopoulos G.D., Alt F.W.;
 RT "Developmentally controlled and tissue-specific expression of
 RT unarranged VH gene segments.";
 RL Cell 40:271-281(1985).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M13787; AAA38499.1; --
 DR PIR; A02029; HVM5A1.
 DR HSP; P01810; 2PBUT.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG-LIKE; 1.
 DR Immunoglobulin V region; Signal.
 KW SIGNAL
 FT CHAIN 1
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH58 A1/A4.
 FT DOMAIN 20 49 FRAMEWORK-1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 68 FRAMEWORK-2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 86 117 FRAMEWORK-3.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON TER 117
 SQ SEQUENCE 117 AA; 12971 MW; 8B0BC138856DFC9D CRC64;
 Query Match 33.1%; Score 423; DB 1; Length 117;
 Best Local Similarity 79.0%; Pred. No. 3.5e-26;
 Matches 83; Conservative 6; Mismatches 16; Indels 0; Gaps 0;
 QY 122 GGGGSEVQLOQSGPELVKPGASVKISCDKSGYAFNMMWVKRPGGGLMIGRIYP 181
 DB 13 GTAGVHCQVQLOQSGPELVKPGALVKISCRASGYTFSTYDINWVKRPGGGLMIGRIYP 72
 QY 182 GGGGSEVQLOQSGPELVKPGASVKISCDKSGYAFNMMWVKRPGGGLMIGRIYP 226
 DB 73 GGGGSEVQLOQSGPELVKPGALVKISCRASGYTFSTYDINWVKRPGGGLMIGRIYP 117
 Db 73 GGGGSEVQLOQSGPELVKPGALVKISCRASGYTFSTYDINWVKRPGGGLMIGRIYP 117
 RESULT 13
 HVO6 MOUSE
 ID HVO6 MOUSE STANDARD; PRT; 117 AA.
 AC P01750;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 15-JUL-1999 (Rel. 01, last sequence update)
 DT 15-JUL-1999 (Rel. 38, last annotation update)
 DE IG heavy chain V region 102 precursor.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 RN [1]
 RE SEQUENCE FROM N.A.
 RX STRAIN=C57BL/6;
 RX MEDLINE=81234548; PubMed=6788376;
 RA Bothwell A.L.M., Peakind M., Reth M., Imanishi-Kari T., Rajewsky K.,

RA Baltimore D.;
 RT "Heavy chain variable region contribution to the Npb family of
 RT antibodies: somatic mutation evident in a gamma 2a variable region";
 RL Cell 24:625-637(1981).
 CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
 CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
 CC PIR; A02032; HVM502.
 DR HSP; P01810; 2PBUT.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG-LIKE; 1.
 KW Immunoglobulin V region; Signal.
 FT CHAIN 1
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 102.
 FT DOMAIN 20 49 FRAMEWORK-1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 68 FRAMEWORK-2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 86 117 FRAMEWORK-3.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON TER 117
 SQ SEQUENCE 117 AA; 12867 MW; 740A65D851FC8C CRC64;
 Query Match 32.0%; Score 421; DB 1; Length 117;
 Best Local Similarity 79.2%; Pred. No. 5e-26;
 Matches 80; Conservative 6; Mismatches 15; Indels 0; Gaps 0;
 QY 125 GGGSEVQLOQSGPELVKPGASVKISCDKSGYAFNMMWVKRPGGGLMIGRIYP 184
 DB 16 GVSHVQLOQSGPELVKPGASVKISCRASGYTFSTYDINWVKRPGGGLMIGRIYP 75
 QY 185 DSNYNGKFKPKKATLTADKSSSTAYWQSLSTVSAYVYFCA 225
 DB 76 DSNYNGKFKPKKATLTADKSSSTAYWQSLSTVSAYVYFCA 116
 Db 76 DSNYNGKFKPKKATLTADKSSSTAYWQSLSTVSAYVYFCA 116
 RESULT 14
 HVA8 MOUSE
 ID HVA8 MOUSE STANDARD; PRT; 138 AA.
 AC P03980;
 DT 23-OCT-1986 (Rel. 02, Created)
 DT 23-OCT-1986 (Rel. 02, last sequence update)
 DT 15-JUL-1999 (Rel. 38, last annotation update)
 DE IG heavy chain V region TPC 1017 precursor.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 RN [1]
 RE SEQUENCE FROM N.A.
 RX MEDLINE=84248078; PubMed=6429663;
 RX Gilliam A.C., Shen A., Richards J.B., Blattner F.R., Mushinski J.F.,
 RA Tucker P.W.;
 RT "Illegitimate recombination generates a class switch from C mu to C
 RT delta in an Igd-secreting plasmacytoma.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
 DR PIR; A02033; HVM57.
 DR HSP; P01810; 2PBUT.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG-LIKE; 1.
 KW Immunoglobulin V region; Signal.
 FT CHAIN 1
 FT CHAIN 21 138 IG HEAVY CHAIN V REGION TPC 1017.
 FT DOMAIN 21 49 FRAMEWORK-1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 68 FRAMEWORK-2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 86 117 FRAMEWORK-3.

FT DOMAIN 118 127 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 128 138 FRAMEWORK-4.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON_TER 138 138
 SQ SEQUENCE 138 AA; 15576 MW; 748157E4C6907B8E CRC64;

Query Match 31.8%; Score 419; DB 1; Length 138;
 Best Local Similarity 68.3%; Pred. No. 8.6e-26;
 Matches 82; Conservative 11; Mismatches 27; Indels 0; Gaps 0;

QY 128 SEVQLQSGPELVKPGASVKISCKDGYAFNNSGMNWVKORPPQGLEWIGRIYPGDGSN 187
 DB 19 SCVQLQPGAEIVKPGASVYQISCKASGHTFTYWIHWIKORPPQGLEWIGRIYPGDGRN 78
 QY 188 YNKEFKGKAITLADKSSSTAYVQSLTSVDSAVYFCARSGILRYAMDYWGQTSVTSS 247
 DB 79 YNKEFKGKAITLTVKSSSTAYVQSLTSVDSAVYFCARSDGYIDMFVWGQTLVTFSA 138

RESULT 15
 ID HV13 MOUSE STANDARD; PRT; 117 AA.
 AC P01757;
 DT 21-UTL-1986 (Rel. 01, Created)
 DT 21-UTL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region J558.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_taxid=10090;
 RN [1]
 RP SEQUENCE.
 RA MEDLINE=80078170; PubMed=6765983;
 RA Schilling J., Clevinger B., Davis J.M., Hood L.;
 RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
 RT rearrangements in heavy chain V-region gene segments.",
 RL Nature 283:35-40(1980). SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
 CC -1- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
 CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
 CC WHICH OCCUR IN THE D AND J SEGMENTS.
 CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE DOMAIN.
 CC PIR: A26242; MEMSJS.
 DR HESP; P01789; 1MCP.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IgV_1.
 DR PROSITE; PS50835; Ig LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 116 IG-LIKE.
 FT DISULFID 22 96 BY SIMILARITY.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;

Query Match 31.5%; Score 415; DB 1; Length 117;
 Best Local Similarity 70.0%; Pred. No. 1.5e-25;
 Matches 84; Conservative 10; Mismatches 22; Indels 4; Gaps 2;

QY 129 EYQLQSGPELVKPGASVKISCKDGYAFNNSGMNWVKORPPQGLEWIGRIYPGDGSN 188
 DB 1 EYQLQSGPELVKPGASVKISCKASGYFTDYMKVVKQSHGKLEWIGIDINPNNGTSTY 60
 QY 189 NGKEFKGKAITLADKSSSTAYVQSLTSVDSAVYFCARSGILRYAMDYWGQTSVTSS 247
 DB 61 NGKEFKGKAITLTVKSSSTAYVQSLTSVDSAVYFCARD--RYWTFDYGAGTIVVSS 117

A:Residues: 1-119 <WTN>
A:Molecule type: DNA

F:36-49/Region: framework 2
 F:50-66/Region: complementarity-determining 2
 F:67-98/Region: framework 3
 F:99-110/Region: complementarity-determining 3
 F:111-118/Region: framework 4

Query Match 39.9%; Score 526; DB 2; Length 118;
 Best Local Similarity 84.7%; Pred. No. 4.7e-29;
 Matches 100; Conservative 7; Mismatches 9; Indels 2; Gaps 1;

QY 129 EVLOOQSGPELVKPGASVKISCKDGYAFNSGMMWVVKRPQGLWMIRITPPGDDSNY 188
 DB 1 QVLOOQSGPELVKPGASVKISCKASGYAFSSMMWVVKRPQGLWMIRITPPGDDSNY 60
 DB 189 NGKFEKALITLADKSSSTAYMQLSLTSVDSAVYFCASGLRLRYAMD--YWGQTSVT 244
 61 NGKFKKATLTADKSSSTAYMQLSLTSVDSAVYFCASGLRLGLPRAYWGQTSVT 118

RESULT 7
 A29380
 Ig kappa chain precursor V region (AC-1001) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 21-Jan-2000
 C:Accession: A29380
 R:Chen, H.T.; Kabat, E.A.; Lundblad, A.; Ratcliffe, R.M.
 J. Biol. Chem. 262, 13579-13583, 1987
 A:Title: Nucleotide and translated amino acid sequences of cDNA coding for the variable
 A:Reference number: A92612; MUID:88007582; PMID:3115981
 A:Accession: A29380
 A:Molecule type: mRNA
 A:Residues: 1-122 <CHS>
 A:Cross-references: GB:M17160; GB:J02815; NID:g196895; PIDN:AAA38824.1; PID:g196896
 A:Note: the authors translated the codon TTC for residue 1 as Leu
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:30-104/Domain: immunoglobulin homology <IMM>

Query Match 39.9%; Score 525; DB 2; Length 122;
 Best Local Similarity 91.7%; Pred. No. 5.6e-29;
 Matches 99; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQTSSLSASLGRVTVSCRASQDINRYLNWYQKRPDGVKFLIYYSRLQGVPS 60
 DB 15 DIQMTQTSSLSASLGRVTVSCRASQDINRYLNWYQKRPDGVKFLIYYSRLQGVPS 74
 QY 61 RFGSGSGTDYSLTINLEQEDIGTYFCQCGNTPPWTFGGGTLKLEIKR 108
 DB 75 RFGSGSGTDYSLTINLEQEDIGTYFCQCGNTLPWTFGGGTLKLEIKR 122

RESULT 8
 P10235
 Ig heavy chain V region (anti-DNA, 2F2VH and 4H8VH) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
 C:Accession: P10235
 R:Shlomchik, M.; Maccelelli, M.; Shan, H.; Radic, M.Z.; Plisetsky, D.; Marehak-Rochstein, A.
 J. Exp. Med. 171, 285-297, 1990
 A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
 A:Reference number: P10231; MUID:90111618; PMID:2104919
 A:Accession: P10235
 A:Molecule type: mRNA
 A:Residues: 1-117 <SHL>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:1-30/Region: framework 1
 F:15-98/Domain: immunoglobulin homology <IMM>
 F:31-35/Region: complementarity-determining 1
 F:36-49/Region: framework 2
 F:50-66/Region: complementarity-determining 2
 F:67-98/Region: framework 3
 F:99-109/Region: complementarity-determining 3

F:110-117/Region: framework 4

Query Match 39.8%; Score 524.5; DB 2; Length 117;
 Best Local Similarity 84.6%; Pred. No. 5.8e-29;
 Matches 99; Conservative 7; Mismatches 10; Indels 1; Gaps 1;

QY 129 EVLOOQSGPELVKPGASVKISCKDGYAFNSGMMWVVKRPQGLWMIRITPPGDDSNY 188
 DB 1 QVLOOQSGPELVKPGASVKISCKASGYAFSSMMWVVKRPQGLWMIRITPPGDDSNY 60
 DB 189 NGKFEKALITLADKSSSTAYMQLSLTSVDSAVYFCASGLRLRYAMD--YWGQTSVT 244
 61 NGKFKKATLTADKSSSTAYMQLSLTSVDSAVYFCASGLRLGLPRAYWGQTSVT 117

RESULT 9
 S69903
 Ig kappa chain (clone KL2.29 / KL2.33 / KL3.8) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
 C:Accession: S69903; S69904; S69905
 R:Wysoczk, L.J.; Creason, G.; Lehmann, K.R.; Cambier, J.C.
 Immunology 75, 116-121, 1992
 A:Title: B-cell proliferation initiated by Ia cross-linking and sustained by interleukin
 A:Reference number: S69900; MUID:92165291; PMID:1537587
 A:Accession: S69903
 A:Status: preliminary; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-108 <WYS>
 A:Cross-references: EMBL:X55044; NID:g511029; PIDN:CAA38884.1; PID:g511030
 A:Accession: S69904
 A:Status: preliminary; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-108 <WT2>
 A:Cross-references: EMBL:X55045; NID:g511031; PIDN:CAA38885.1; PID:g511032
 A:Accession: S69905
 A:Status: preliminary; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-108 <WT3>
 A:Cross-references: EMBL:X55046; NID:g511033; PIDN:CAA38886.1; PID:g511034
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 39.5%; Score 520; DB 2; Length 108;
 Best Local Similarity 91.7%; Pred. No. 1.1e-28;
 Matches 99; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQTSSLSASLGRVTVSCRASQDINRYLNWYQKRPDGVKFLIYYSRLQGVPS 60
 DB 1 DIQMTQTSSLSASLGRVTVSCRASQDINRYLNWYQKRPDGVKFLIYYSRLQGVPS 60
 QY 61 RFGSGSGTDYSLTINLEQEDIGTYFCQCGNTPPWTFGGGTLKLEIKR 108
 DB 61 RFGSGSGTDYSLTINLEQEDIGTYFCQCGNTLPWTFGGGTLKLEIKR 108

RESULT 10
 J10080
 Ig kappa chain precursor V region (anti-phenylloxazalone, 18C10) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 21-Jan-2000
 C:Accession: J10080
 R:Kaartinen, M.; Rocca-Serra, J.; Maekelae, O.
 Mol. Immunol. 25, 859-865, 1988
 A:Title: Combinatorial association of V genes: one VH gene codes for three non-cross-ree
 A:Reference number: J10076; MUID:89069973; PMID:3211160
 A:Accession: J10080
 A:Molecule type: mRNA
 A:Residues: 1-115 <KAA>
 A:Cross-references: GB:M27793; NID:g197161; PIDN:AAA3937.1; PID:g197162
 A:Note: the authors translated the codon AGG for residue 30 as Ser
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: immunoglobulin

F/1-6/Domain: signal sequence (fragment) #status predicted <SIG>
F/7-115/Product: Ig light chain #status predicted <MAT>
F/22-96/Domain: immunoglobulin homology <IMM>
F/30-40/Region: complementarity-determining 1
F/56-62/Region: complementarity-determining 2

Query Match 39.5%; Score 520; DB 2; Length 115;
Best Local Similarity 91.7%; Pred. No. 1.2e-28;
Matches 99; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIOMTQTSSLSASLGDRVTSCRASODIRNYLNWYQOKPDGTVKFLIYTSRLQGPVS 60
DB 7 DIOMTQTSSLSASLGDRVTSCRASODIRNYLNWYQOKPDGTVKFLIYTSRLHSGVPS 66
QY 61 RFSGSGSGTDYSLTINLLEQEDIGTYFCQOGNTPMTFGGCTKLEIKR 108
DB 67 RFSGSGSGTDYSLTINLLEQEDIGTYFCQOGNTPMTFGGCTKLEIKR 114

RESULT 11

IG kappa chain V region - mouse
C/Species: Mus musculus (house mouse)
C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C/Accession: S38862
R/Fischer, R.; Voss, A.; Hunziker, W.; Stierhof, Y.D.; Kreuzaler, F.
submitted to the EMBL Data Library, August 1993
A/Description: Production and cloning of TMV-specific monoclonal antibodies.
A/Reference number: S37200
A/Accession: S38862
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-108 <FIS>
A/Cross-references: EMBL:X75854; NID:G429109; PID:G429110
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/16-90/Domain: immunoglobulin homology <IMM>

Query Match 39.4%; Score 519.5; DB 2; Length 108;
Best Local Similarity 90.7%; Pred. No. 1.2e-26;
Matches 99; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

QY 1 DIOMTQTSSLSASLGDRVTSCRASODIRNYLNWYQOKPDGTVKFLIYTSRLQGPVS 60
DB 1 DIOMTQTSSLSASLGDRVTSCRASODIRNYLNWYQOKPDGTVKFLIYTSRLHSGVPS 60

QY 61 RFSGSGSGTDYSLTINLLEQEDIGTYFCQOGNTPMTFGGCTKLEIKR 107
DB 61 RFSGSGSGTDYSLTINLLEQEDIGTYFCQOGNTPMTFGGCTKLEIKR 108

RESULT 12

IG kappa chain precursor V region (5-27) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 21-Jan-2000
C/Accession: A34904
R/Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
J. Biol. Chem. 265, 133-138, 1990
A/Title: Active site structure and antigen binding properties of idiotypically cross-reactive antibodies: heterotetramer; immunoglobulin
A/Reference number: A34903; MUID:90094387; PMID:2104617
A/Accession: A34904
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-126 <BED>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/35-109/Domain: immunoglobulin homology <IMM>

Query Match 39.3%; Score 518; DB 2; Length 126;
Best Local Similarity 92.5%; Pred. No. 1.7e-28;
Matches 98; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIOMTQTSSLSASLGDRVTSCRASODIRNYLNWYQOKPDGTVKFLIYTSRLQGPVS 60
DB 20 DIOMTQTSSLSASLGDRVTSCRASODIRNYLNWYQOKPDGTVKFLIYTSRLHSGVPS 79
QY 61 RFSGSGSGTDYSLTINLLEQEDIGTYFCQOGNTPMTFGGCTKLEIKR 106
DB 80 RFSGSGSGTDYSLTINLLEQEDIGTYFCQOGNTPMTFGGCTKLEIKR 125

RESULT 13

PI0234
IG heavy chain V region (anti-DNA, 3H9VH) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
C/Accession: PI0234
R/Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Plesetsky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990
A/Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic hypermutation
A/Reference number: PI0231; MUID:9011618; PMID:2104919
A/Accession: PI0234
A/Molecule type: mRNA
A/Residues: 1-117 <SHL>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/1-30/Region: framework 1
F/15-98/Domain: immunoglobulin homology <IMM>
F/31-35/Region: complementarity-determining 1
F/36-49/Region: framework 2
F/50-66/Region: complementarity-determining 2
F/67-98/Region: framework 3
F/99-109/Region: complementarity-determining 3
F/110-117/Region: framework 4

Query Match 39.1%; Score 515.5; DB 2; Length 117;
Best Local Similarity 84.6%; Pred. No. 2.4e-28;
Matches 99; Conservative 5; Mismatches 12; Indels 1; Gaps 1;

QY 129 EVOLQSGPELVKGAQVKTSCDQGYAFNSMWNWYQOKPDGTVKFLIYTSRLQGPVS 188
DB 1 QVQIQSGPELVKGAQVKTSCDQGYAFNSMWNWYQOKPDGTVKFLIYTSRLQGPVS 60

QY 189 NGKFEGRKILTDAGSSSTAYVQLSSTVSVAIVFCARLGLRIYANDYGGGTSVT 244
DB 61 NGKFEGRKILTDAGSSSTAYVQLSSTVSVAIVFCARLGLRIYANDYGGGTSVT 117

RESULT 14

IG kappa chain (clone KL2.21) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C/Accession: S69901
R/Wysocki, L.J.; Creighton, G.; Lehmann, K.R.; Cambier, J.C.
Immunology 75, 116-121, 1992
A/Title: B-cell proliferation initiated by Ia cross-linking and sustained by interleukin 4
A/Reference number: S69900; MUID:92165291; PMID:1557587
A/Accession: S69901
A/Status: preliminary; translation not shown
A/Molecule type: DNA
A/Residues: 1-107 <WYS>
A/Cross-references: EMBL:X55042; NID:G511025; PID:CAA38862.1; PID:G511026
F/16-90/Domain: immunoglobulin V region; immunoglobulin homology <IMM>

Query Match 38.8%; Score 511.5; DB 2; Length 107;
Best Local Similarity 91.7%; Pred. No. 4e-28;
Matches 99; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

QY 1 DIOMTQTSSLSASLGDRVTSCRASODIRNYLNWYQOKPDGTVKFLIYTSRLQGPVS 60
DB 1 DIOMTQTSSLSASLGDRVTSCRASODIRNYLNWYQOKPDGTVKFLIYTSRLHSGVPS 60
QY 61 RFSGSGSGTDYSLTINLLEQEDIGTYFCQOGNTPMTFGGCTKLEIKR 108

Db 61 RFGSGSGTDYSLTISNLEQEDIAITYFCQGNLT-LMTFEGGTYLEIKR 107

RESULT 15

KWSAR

Ig kappa chain V regions (anti-arsenate hybridoma proteins) - mouse

C/Species: Mus musculus (house mouse)

C/Date: 06-Jul-1982 #sequence_revision 06-Jul-1982 #text_change 21-Jan-2000

C/Accession: A01927

R/Siegelman, M.; Capra, J.D.

Proc. Natl. Acad. Sci. U.S.A. 78, 7679-7683, 1981

A/Title: Complete amino acid sequence of light chain variable regions derived from five

A/Reference number: A01927; MID:82150934; PMID:6801658

A/Accession: A01927

A/Molecule type: protein

A/Residues: 1-108 <SIB>

A/Experimental source: strain A/U

A/Note: hp 93G7 differs in having 93-Met; HP 123E6 differs in having 7-Ser, 92-Tyr, and

Arg, 84-Ser, and 93-Ala

C/Comment: The sequence shown is HP R16.7.

C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)

chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer

F/16-90/Domain: immunoglobulin homology <IMM>

F/23-88/Disulfide bonds: #status predicted

Query Match 38.8%; Score 511; DB 1; Length 108;
Best Local Similarity 90.7%; Pred. No. 4.4e-28;
Matches 98; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIQMTQTSLSASLSDRVTVSCRASQDINRYLAWYQKPKDGVKFLIYYTSRLQGVPS 60
Db 1 DIQMTQTSLSASLSDRVTVSCRASQDINRYLAWYQKPKDGVKFLIYYTSRLHSGVPS 60

QY 61 RFGSGSGTDYSLTINNLEQEDIGTYFCQGNTPPMTFEGGTYLEIKR 108
Db 61 RFGSGSGTDYSLTISNLEQEDIAITYFCQGNSTPRTFEGGTYLEIKR 108

Search completed: April 22, 2004, 11:57:11
Job time: 14 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 22, 2004, 11:45:27 ; Search time 51 Seconds
(without alignments)

1368.416 Million cell updates/sec

Title: US-10-620-049-23
Perfect score: 1317
Sequence: 1 DIQMTQYTSLSASLGRVT.....GLRYPADYWGQGRSVTVSS 247

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp19808:*
2: geneseqp19908:*
3: geneseqp20008:*
4: geneseqp20018:*
5: geneseqp20028:*
6: geneseqp20038:*
7: geneseqp20038:*
8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1250	94.9	247	6	AAO27253
2	1249	94.8	247	6	AAO27253
3	1243	94.3	247	6	AAO27252
4	1240	94.2	247	6	AAO27254
5	1237	93.9	247	6	AAO27256
6	994	75.5	637	5	AAU75365
7	994	75.5	637	5	AAU75370
8	994	75.5	656	5	AAU75383
9	994	75.5	657	5	AAU75389
10	992	75.3	601	3	AAO27461
11	992	75.3	601	3	AAO27461
12	992	75.3	642	5	AAU75382
13	992	75.3	642	5	AAU75382
14	992	75.3	643	5	AAU75390
15	992	75.3	643	5	AAO29670
16	988.5	75.1	895	5	AAU75369
17	988.5	75.1	895	5	AAU75369
18	988.5	75.1	895	5	AAU75374
19	988.5	75.1	895	5	AAU75374
20	988.5	75.1	896	5	AAU75367
21	988.5	75.1	896	5	AAU75366
22	988.5	75.1	896	5	AAU75373
23	988.5	75.1	896	5	AAU75373
24	988.5	75.1	896	6	AAO29671
25	988.5	75.1	896	6	AAO29676

26	988.5	75.1	899	5	AAU75375	AAU75375	Diphtheri
27	988.5	75.1	899	5	AAO29674	AAO29674	Anti-T ce
28	984.5	74.8	652	5	AAU75448	AAU75448	Immunotox
29	954	72.4	302	2	AAO60206	AAO60206	Bispecific
30	953.5	72.4	554	3	AAU50822	AAU50822	Fv-antibo
31	948	72.0	504	7	ADD25787	ADD25787	Binding d
32	948	72.0	555	7	ADBE6039	ADBE6039	Anti-CD3
33	924	70.2	562	6	ABR57058	ABR57058	Plasmiid p
34	920.5	69.9	531	3	AAU43749	AAU43749	Amino aci
35	911	69.2	271	5	ABG31022	ABG31022	Mouse sin
36	911	69.2	271	7	ADD25451	ADD25451	Binding d
37	895	68.0	251	4	AAU74793	AAU74793	Single ch
38	895	68.0	258	4	AAU74794	AAU74794	Single ch
39	888	67.4	543	7	ADD12876	ADD12876	CD28/me1a
40	881	66.9	507	5	AAU72858	AAU72858	BG7C10x4-
41	868	65.9	539	3	AAU50823	AAU50823	Fv-antibo
42	866	65.8	562	6	ABR57059	ABR57059	Plasmiid p
43	851.5	64.7	436	3	AAU91026	AAU91026	Apoptobod
44	848	64.4	650	6	ABR62591	ABR62591	Anti-CD7
45	848	64.4	651	6	ABR62590	ABR62590	Anti-CD7

ALIGNMENTS

RESULT 1	AAO27253	AAO27253 standard; protein; 247 AA.
ID	AAO27253	
XX	AAO27253	
AC	AAO27253	
XX	17-SEP-2003	(first entry)
DE	Antibody 14B7 scFv mutant A2E amino acid sequence.	
XX	Mouse, murine; affinity-matured recombinant antibody;	
KM	proteolaseous toxin; Bacillus anthracis protective antigen;	
KM	antibacterial; gene therapy; vaccine; biological warfare agent;	
XX	infection; hybridoma; scFv; 14B7; mutant; mutein; A2E.	
XX	Mus SP.	
OS	Synthetic.	
XX		
FT	Key	Location/Qualifiers
FT	Region	1..108
FT	Region	/label= Light_chain
FT	Region	1..23
FT	Region	/label= LFR1
FT	Region	/note= "Light chain framework region 1"
FT	Region	24..34
FT	Region	/label= CDR_L1
FT	Region	/note= "Complementarity determining region L1"
FT	Region	35..49
FT	Region	/label= LFR2
FT	Region	/note= "Light chain framework region 2"
FT	Region	50..56
FT	Region	/label= CDR_L2
FT	Region	/note= "Complementarity determining region L2"
FT	Region	56
FT	Region	/note= "Wild-type Ser substituted by Pro"
FT	Region	57..88
FT	Region	/label= LFR3
FT	Region	/note= "Light chain framework region 3"
FT	Region	89..97
FT	Region	/label= CDR_L3
FT	Region	/note= "Complementarity determining region L3"
FT	Region	98..108
FT	Region	/label= LFR4
FT	Region	/note= "Light chain framework region 4"
FT	Region	109..128
FT	Region	/label= linker
FT	Region	/note= "(GlySer)4 linker"
FT	Region	129..247

FT	Region	/label= Heavy_chain
FT		129. .154
FT		/label= HFR1
FT	Region	/note= "Heavy chain framework region 1"
FT		155. .163
FT		/label= CDR H1
FT	Region	/note= "Complementarity determining region H1"
FT		164. .177
FT		/label= HFR2
FT		/note= "Heavy chain framework region 2"
FT	Region	178. .194
FT		/label= CDR H2
FT	Region	/note= "Complementarity determining region H2"
FT		195. .226
FT		/label= HFR3
FT	Region	/note= "Heavy chain framework region 3"
FT		227. .236
FT		/label= CDR H3
FT	Region	/note= "Complementarity determining region H3"
FT		237. .247
FT		/label= HFR4
FT	Region	/note= "Heavy chain framework region 4"

W02003040384-A1.

15-MAY-2003

05-NOV-2002; 2002WO-US035567.

05-NOV-2001; 2001US-0332849P.

(TEXA) UNIV TEXAS SYSTEM.

Georgiou G, Iverson BL, Maynard JA,

WPI; 2003-430672/40.

New purified affinity-matured recombinant antibody with binding specificity for *Bacillus anthracis* protective antigen, useful for diagnosing, preventing or treating anthrax or other bacterial infections

CC This invention relates a purified affinity-matched recombinant antibody
CC or its portion having binding specificity for a proteinaceous toxin or a
CC Bacillus anthracis protective antigen. The antibody may have an
CC antibacterial activity and may be used in gene therapy of a vaccine.
CC Bacillus anthracis, commonly referred to as one of the first
CC biological warfare agents to be developed and is now perceived as a major
CC threat worldwide. The composition and methods of the invention may be
CC useful in diagnosing, preventing or treating infections caused by
CC Bacillus anthracis and other bacterial toxins. The present sequence is
CC that of the mouse wild-type anti-protective antigen hybridoma antibody
CC 1A87 scFv mutant A2E, with a synthetic linker (GlySer)₄ between the
CC light and heavy chains. This antibody had a Ser56Pro substitution
CC compared to the wild-type sequence (see PA027252) and was developed in
CC the examples of the specification in order to identify antibodies which
CC had increased binding affinity for the Bacillus anthracis toxin. Note:
CC This sequence does not appear in the specification but was created by the
CC indexer using information given in the examples and figure 4 of the
CC disclosure

SQ Sequence 247 AA;

Query Match 94.9%; Score 1250; DB 6; Length 247;

Matches 235; Conservative 5; Mismatches 7; Indels 0; Gaps 0

QY 1 DIQMTQTSSLSASLGDRVTVSCRASQDIRNYLNWYQOKPDGTVKFLIYTSRLQPGVPS 60

Db 1 DIQMIQTSSLASLGDRVTISCRASQDIRNYLNWYQQKPDGTVKLLIYYTSRLQPGVPS 60

Db	61	RFGSGSSGTDYSLTISNQEDIGTYFCQGNLTLPWFGGATKLEIRGGGGSGGGSGG	120
Qy	121	GGSGGGGGSEVQIQSGSPELVYKPGASVKISCHDSGYAANSMMWVKRPGQGLEWGR	180
Db	121	GGSGGGGGSEVQIQSGSPELVYKPGASVKISCHDSGYAASSMMWVKRPGQGLMIR	180
Qy	181	PGDGDNNYKGEKRAIITADKSSGTAYMQLSSTLYSDSAVYFCARSGLLRYAMDYGGG	240
Db	181	PGDGDNNYKGEKRAIITADKSSGTAYMQLSSTLYSDSAVYFCARSGLLRYAMDYGGG	240
Qy	241	TSYTVSS	247
Db	241	TSYTVSS	247

RESULT 2

ID AA027255 standard; protein; 247 AA.

AC AA027255;

DT 17-SEP-2003 (first entry)

DE. Antibody 14B7 scFv mutant 6A amino acid sequence.

KW Mouse; murine; affinity-matured recombinant antibody;

KW antibacterial; gene therapy; vaccine; biological warfare agents

XX

OS Synthetic.

FH	Key	Location/Qualifiers
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4	4	4
5	5	5
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FT /label= light chain
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ET /label= LFR1

Region	24. .34
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/note= "Complementarity determining region L1"

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:
: /label= LFR2
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: FT

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99	0.0000	0.00
100	0.0000	0.00

Region	50	.56
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11 /note= "Complementarity determining region 1,2"
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FT MIBC-REFERENCE 30 /not-a- "wild-type Ser substituted by Pro"

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region
2/1: .00
/label = T.FB3

BT	Section
F1	/1106 = "MAYNUT CHADIN L'ADAMWONZ" 2
89	97

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F1      /label= CDR_D3
FT      /note= "Commentary: determining reaction T3"

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FT	38. :106
F1	/12601~ TFB4
F1	Region

ET	Position	109	128
ET	/note= "Light chain framework region 4"		

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F1 /label= LINKEL
FT /noto= "(/C1)w4Sec) 1 144nbor"

```

F1 MISC-DIFFERENCE 118
/2000- WWD-time car substituted by Thx

Region	Label = Hoare's chain
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F1	Region	129. :134
ET		/label = YFR1

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FT FT /label= CDR H1
FT FT /note= "Complementarity determining region H1"
FT Region 164..177
FT FT /label= HFR2
FT FT /note= "Heavy chain framework region 2"
FT Region 178..194
FT FT /label= CDR H2
FT FT /note= "Complementarity determining region H2"
FT Region 195..226
FT FT /label= HFR3
FT FT /note= "Heavy chain framework region 3"
FT Misc-difference 207
FT FT /note= "Wild-type Ala substituted by Glu"
FT Region 227..236
FT FT /label= CDR H3
FT FT /note= "Complementarity determining region H3"
FT Region 237..247
FT FT /label= HFR4
FT FT /note= "Heavy chain framework region 4"
XX XX WO2003040384-A1.
XX PN
XX PD 15-MAY-2003.
XX XX
XX PP 05-NOV-2002; 2002WO-US035567.
XX XX
XX PR 05-NOV-2001; 2001US-0332849P.
XX XX
XX PA (TEXA) UNIV TEXAS SYSTEM.
XX XX
PI Georgiou G, Iverson BL, Maynard JA;
DR WPI; 2003-430672/40.
XX XX
PT New purified affinity-matured recombinant antibody with binding
XX specificity for Bacillus anthracis protective antigen, useful for
XX diagnosing, preventing or treating anthrax or other bacterial infections.
PS Example; Page: 48pp; English.

This invention relates a purified affinity-matured recombinant antibody or its portion having binding specificity for a proteinaceous toxin or a Bacillus anthracis protective antigen. The antibody may have an antibacterial activity and may be used in gene therapy or a vaccine. Bacillus anthracis, commonly referred to as was one of the first biological warfare agents to be developed and is now perceived as a major threat worldwide. The composition and methods of the invention may be useful in diagnosing, preventing or treating infections caused by Bacillus anthracis and other bacterial toxins. The present sequence is that of the mouse wild-type anti-protective antigen hybridoma antibody 14B7 scFv mutant 6A, with a synthetic linker (Gly4Ser)4 between the light and heavy chains. This antibody had Leu46Phe, Ser56Pro, Ser18Thr and Ala207Glu substitutions compared to the wild-type sequence (see A402752) and was developed in the examples of the specification in order to identify antibodies which had increased binding affinity for the Bacillus anthracis toxin. Note: This sequence does not appear in the specification but was created by the indexer using information given in the examples and Figure 4 of the disclosure

Query Match	94.8%	Score 1249;	DB 6;	Length 247;
Best Local Similarity	94.7%	Pred. No 2,1e-76;		
Matches 234; Conservative	6;	Mismatches 7;	Indels 0;	Gaps 0

QY 1 DIQMTQTSTSLASLIGRVTASCRASODIRNYINMYQCPDQTVFLIYYSRLQPGVPS 60
Db 1 DIQMQTSSLASLIGRVTISCRASODIRNYINMYQCPDQTVFLIYYSRLQPGVPS 60
QY 61 RPSGSGSTDYSLFINLLEQEDIGYFCCQGNPPTFGGKRLKIKKGGGSGDGGGSGG 120
Db 61 RPSGSGSTDYSLFINLLEQEDIGYFCCQGNPPTFGGKRLKIKKGGGSGDGGGSGG 120

Oy		122	GSGGGGSEVCOQSGPELVKPGASVKISKCDSDGYAFNSYMMWVKQRPCGGLEIMIRIY	160
Dd		121	GSGGGGSEVCOQSGPELVKPGASVKISKCDSDGYAFNSYMMWVKQRPCGGLEIMIRIY	160
Oy		181	PGDGSNNGKEEGKALITADKSSTAYMQLSLTYSVDNAVFCARAGLLRYANDYWGOG	240
Dd		181	PGDGDTNYNGEKERATLTADKSSSTGYMLSSLTSYSDNAVFCARSGLLRYANDYWGOG	240
Oy		241	TSYTASS 247	
Dd		241	TSYTASS 247	
RESULT 3				
ID	AAO27252	standard; protein; 247 AA.		
XX	AAO27252;			
AC				
XX	17-SEP-2003	(first entry)		
DT				
XX				
DE	Antibody 14B7 scFv wild type amino acid sequence.			
KX				
KM	Mouse; murine; affinity-matured recombinant antibody;			
KW	proteinnaceous toxin; Bacillus anthracis protective antigen;			
KM	antibacterial; gene therapy; vaccine; biological warfare agent;			
KX	infection; hybridoma; scFv; 14B7.			
OS	Mus sp.			
OS	Synthetic.			
FH	Key	Location/Qualifiers		
FT	Region	1..108		
FT		/label= Light_chain		
FT	Region	1..23		
FT		/label= LFR1		
FT		/note= "light chain framework region 1"		
FT	Region	24..34		
FT		/label= CDR_L1		
FT		/note= "Complementarity determining region L1"		
FT		35..49		
FT		/label= LFR2		
FT		/note= "light chain framework region 2"		
FT	Region	50..56		
FT		/label= CDR_L2		
FT		/note= "Complementarity determining region L2"		
FT		57..88		
FT		/label= LFR3		
FT		/note= "light chain framework region 3"		
FT		89..97		
FT		/label= CDR_L3		
FT		/note= "Complementarity determining region L3"		
FT	Region	98..108		
FT		/label= LFR4		
FT		/note= "light chain framework region 4"		
FT		109..128		
FT		/label= linker		
FT		/note= "(GlySer)4 linker"		
FT	Region	129..247		
FT		/label= Heavy_chain		
FT		129..154		
FT		/label= HFR1		
FT		/note= "Heavy chain framework region 1"		
FT		155..163		
FT		/label= CDR_H1		
FT		/note= "Complementarity determining region H1"		
FT	Region	164..177		
FT		/label= HFR2		
FT		/note= "Heavy chain framework region 2"		
FT		178..194		
FT		/label= CDR_H2		
FT		/note= "Complementarity determining region H2"		
FT	Region	195..226		

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Page 4

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FT FT /label= HFR3
FT FT /note="Heavy chain framework region 3"
FT FT Region
FT FT 227..236
FT FT /label= CDR H3
FT FT /note="Complementarity determining region H3"
FT FT Region
FT FT 237..247
FT FT /label= HFR4
FT FT /note="Heavy chain framework region 4"
XX XX MO2003040384-AL.
XX XX
XX XX 15-MAY-2003.
XX XX
XX PF 05-NOV-2002; 2002MO-US035567.
XX XX
XX PR 05-NOV-2001; 2001US-0332849P.
XX XX
XX PA (TEXA ) UNIV TEXAS SYSTEM.
XX XX
XX PI Georgetown G, Iverson BL, Maynard JA;
XX XX
XX DR WPI; 2003-430672/40.
XX XX
XX XX New purified affinity-matured recombinant antibody with binding
FT FT specifically for Bacillus anthracis protective antigen, useful for
FT FT diagnosing, preventing or treating anthrax or other bacterial infections.
XX XX
XX PS Example; Fig 4; 48bp; English.
XX XX
CC CC This invention relates a purified affinity-matured recombinant antibody
CC CC or its portion having binding specificity for a proteinoaceous toxin or a
CC CC Bacillus anthracis protective antigen. The antibody may have an
CC CC antibacterial activity and may be used in gene therapy or a vaccine.
CC CC Bacillus anthracis, commonly referred to, as was one of the first
CC CC biological warfare agents to be developed and is now perceived as a major
CC CC threat worldwide. The composition and methods of the invention may be
CC CC useful in diagnosing, preventing or treating infections caused by
CC CC Bacillus anthracis and other bacterial toxins. The present sequence is
CC CC 1487 scFv, with a wild-type anti-protective antigen hybridoma antibody
CC CC chain. This antibody was used for the development of mutant antibodies
CC CC (see AAO27285-6) which had increased binding affinity for the Bacillus
CC CC anthracis toxin in which the examples of the specification
XX XX
XX XX Sequence 247 AA;

```

Query	March	94.3%	Score 1242;	DB 6;	Length 247;
Best Local Similarity		94.7%;	Pred. No. 6, 1e-76;		
Matches 234;	Conservative	5;	Mismatches 8;	Indels 0;	Gaps 0

QY	1	DIDMTQTSSLSASISGDRVTWSCASODIRNVLNNYQOKPDKTVKFLYYTSRLPGVPS	60
Db	1	DIDMTQTSSLSASISGDRVTWSCASODIRNVLNNYQOKPDKTVKFLYYTSRLPGVPS	60
QY	61	RFSGSGSGTDYSLTNNLEQEDIGIFYCCQGNTPWTFPGGTYKEIKKGGSGSGGGSGG	120
Db	61	RFSGSGSGTDYSLTNNLEQEDIGIFYCCQGNTPWTFPGGTYKEIKKGGSGSGGGSGG	120
QY	121	GGSGGGSGSEVQLQDGGPELVKPGASVKISCHDGYAFNFSMMNWTKQRPQGQLEWIGRIY	180
Db	121	GGSGGGSGSEVQLQDGGPELVKPGASVKISCHDGYAFNFSMMNWTKQRPQGQLEWIGRIY	180
QY	181	PGDGSNTNGKEFGKAILTADKSSSTAYVQLSITVSDSAVYFCARSGILLRYAMDYWGQ	240
Db	181	PGDGSNTNGKRGKRAITLADKSSSTAYVQLSITVSDSAVYFCARSGILLRYAMDYWGQ	240
QY	241	TSVTIVSS 247	
Db	241	TSVTIVSS 247	

RESULT 4
AAO27254

ID	AA027254	standard; protein; 247 AA.
XX	AA027254;	
AC		
XX	17-SEP-2003	(first entry)
DT		
XX	Antibody 14B7 scFv mutant 1H amino acid sequence.	
DE		
XX		
XX	Mouse; murine; affinity-matured recombinant antibody;	
XX	proteaceous toxin; Bacillus anthracis protective antigen;	
KW	antibacterial; gene therapy; vaccine; biological warfare agent	
KW	infection; hydrioma; scFv; 14B7; mutant; mutein; 1H.	
XX		
OS	Mus sp.	
OS	Synthetic.	
XX		
FH	Key	Location/Qualifiers
FT	Region	1..108
FT		/label= Light_chain
FT	Region	1..23
FT		/label= LFR1
FT		/note= "Light chain framework region 1"
FT	Region	24..34
FT		/label= CDR L1
FT		/note= "Complementarity determining region L1"
FT	Region	35..49
FT		/label= LFR2
FT		/note= "Light chain framework region 2"
FT	Region	50..56
FT		/label= CDR L2
FT		/note= "Complementarity determining region L2"
FT	Misc-difference	55
FT		/note= "Wild-type Gln substituted by Leu"
FT	Misc-difference	56
FT		/note= "Wild-type Ser substituted by Pro"
FT	Region	57..88
FT		/label= LFR3
FT		/note= "Light chain framework region 3"
FT	Region	89..97
FT		/label= CDR L3
FT		/note= "Complementarity determining region L3"
FT	Region	98..108
FT		/label= LFR4
FT		/note= "Light chain framework region 4"
FT	Misc-difference	107
FT		/note= "Wild-type Lys substituted by Arg"
FT	Region	109..128
FT		/label= Linker
FT		/note= "(Gly4Ser) 4 linker"
FT	Region	129..247
FT		/label= Heavy_chain
FT	Region	129..154
FT		/label= HFR1
FT		/note= "Heavy chain framework region 1"
FT	Region	155..163
FT		/label= CDR H1
FT		/note= "Complementarity determining region H1"
FT	Region	164..177
FT		/label= HFR2
FT		/note= "Heavy chain framework region 2"
FT	Region	178..194
FT		/label= CDR H2
FT		/note= "Complementarity determining region H2"
FT	Region	195..226
FT		/label= HFR3
FT		/note= "Heavy chain framework region 3"
FT	Region	227..236
FT		/label= CDR H3
FT		/note= "Complementarity determining region H3"
FT	Region	237..247
FT		/label= HFR4
FT		/note= "Heavy chain framework region 4"
XX		

RESULT 4
AA027254

AA027254

XX Georgiou G, Iversen BL, Maynard JA;
 XX WPI; 2003-430672/40.
 XX
 PT New purified affinity-matured recombinant antibody with binding
 PT specificity for Bacillus anthracis protective antigen, useful for
 PT diagnosing, preventing or treating anthrax or other bacterial infections.
 XX
 XX Example; Page; 48pp; English.

CC This invention relates a purified affinity-matured recombinant antibody
 CC or its portion having binding specificity for a proteinaceous toxin or a
 CC Bacillus anthracis protective antigen. The antibody may have an
 CC antibacterial activity and may be used in gene therapy or a vaccine.
 CC Bacillus anthracis, commonly referred to as was one of the first
 CC biological warfare agents to be developed and is now perceived as a major
 CC threat worldwide. The composition and methods of the invention may be
 CC useful in diagnosing, preventing or treating infections caused by
 CC Bacillus anthracis and other bacterial toxins. The present sequence is
 CC that of the mouse wild-type anti-protective antigen hydridoma antibody
 CC 14B7 scFv mutant 197, with a synthetic linker (Gly4Ser)4 between the
 CC light and heavy chains. This antibody had a leu259ala substitution
 CC compared to the wild-type sequence (see AA027252) and was developed in
 CC the examples of the specification in order to identify antibodies which
 CC had increased binding affinity for the Bacillus anthracis toxin. Note:
 CC This sequence does not appear in the specification but was created by the
 CC indexer using information given in the examples and figure 4 of the
 CC disclosure
 CC
 XX
 SQ Sequence 247 AA;

Query March 93.9%; Score 1237; DB 6; Length 247;
 Best Local Similarity 94.3%; Pred. No. 1,3e-75;
 Matches 233; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQMTQTSSLSASLGRVTVSCRASODIRNYLWYQKPDGVTKLIIYTSRLQGVPS 60
 DB 1 DIQMTQTSSLSASLGRVTVSCRASODIRNYLWYQKPDGVTKLIIYTSRLQGVPS 60
 QY 61 RFGSGSGGTGYSLTINLBOEDIGTVFCQGNTPMPTFGGCTKLEIKRGGSGSDGGSGSG 120
 DB 61 RFGSGSGGTGYSLTINLBOEDIGTVFCQGNTPMPTFGGCTKLEIKRGGSGSGSDGGSGSG 120
 QY 121 GSGSGSGSEVQLQSGPELVKPGASVKISCKDSGYAFNMMWVMVKRPGQGLEWIGRIY 180
 DB 121 GSGSGSGSEVQLQSGPELVKPGASVKISCKDSGYAFNMMWVMVKRPGQGLEWIGRIY 180
 QY 181 PGSDSDSYNKGFEKRLITADKSSSTAYMQLSSTSDVSAVYCARSGILRYAMDYMGQG 240
 DB 181 PGSDSDSYNKGFEKRLITADKSSSTAYMQLSSTSDVSAVYCARSGILRYAMDYMGQG 240
 QY 241 TSVTVSS 247
 DB 241 TSVTVSS 247

RESULT 6
 AAU75365
 ID AAU75365 standard; protein; 637 AA.

AAU75365;

23-APR-2002 (first entry)

Diphtheria toxin/UCHT1 immunotoxin fusion protein #1.

XX Immunotoxin; pseudomonas exotoxin A; ETA; diphtheria toxin; DT;
 KW cytoestatic; immunosuppressive; immunostimulant; antidiabetic;
 KW antineumatic; antitubercular; anti-HIV; anti-inflammatory;
 KW anti-T cell immunotoxin fusion protein; antibody; UCHT1;
 KW T cell leukemia; lymphoma; graft-versus-host disease; Fv;
 KW autoimmune disease; transplant rejection; systemic lupus erythematosus;

KM type I diabetes; rheumatoid arthritis; myasthenia gravis;
 KM multiple sclerosis; AIDS; acquired immunodeficiency syndrome;
 KM chronic immunosuppression; (Gly4Ser)3 linker.

OS Mus sp.
 OS Corynebacterium diphtheriae.
 OS Synthetic.
 OS Chimeric.
 XX WO200187982-A2.

PD 22-NOV-2001.
 XX 18-MAY-2001; 2001WO-US016125.
 XX 18-MAY-2000; 2000US-00573797.

PA (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS-ERRINDUNGEN VERW GES MBH.
 PA (USHS) US DEPT HEALTH & HUMAN SERVICES.

PI Neville DM, Thompson JT, Hu H, Woo J, Ma S, Hexham JM, Digan ME;
 WPI; 2002-121980/16.

PT New anti-T cell immunotoxin fusion protein comprising a truncated
 PT diphtheria toxin moiety, a connector, and one single chain Fv of the
 PT variable region of a UCHT1 antibody, useful for treating e.g. autoimmune
 PT diseases.

XX Claim 17; Page 259-261; 307pp; English.

CC The invention relates to an anti-T cell immunotoxin fusion protein,
 CC comprising from the amino terminus, a truncated diphtheria toxin moiety,
 CC a connector, and one single chain Fv of the variable region of a UCHT1
 CC antibody. The single chain Fv comprises VL, L, or VH, L is a Gly-Ser
 CC linker, and VL and VH are the variable light and heavy domains of the
 CC anti-CD3 antibody UCHT1. Also included are a nucleic acid encoding the
 CC novel immunotoxin fusion protein, a vector comprising the nucleic acid
 CC and a cell comprising the nucleic acid. The immunotoxin may also be a
 CC pseudomonas endotoxin A (ETA). The immunotoxins are useful for treating T
 CC cell leukemias or lymphomas, graft-versus-host diseases, and autoimmune
 CC diseases by inducing immune tolerance. The immunotoxin fusion proteins
 CC may be used in vivo to systemically reduce populations of T cells, or ex
 CC vivo to effect T-cell depletion from a treated cell population. The
 CC fusion proteins can be administered to a subject who is or will be a
 CC recipient of an allogeneic transplant to prevent or reduce T-cell mediated acute
 CC or chronic transplant rejection of the transplant allogeneic cells,
 CC tissue or organ in the subject as well as treat other T-cell mediated
 CC diseases such as systemic lupus erythematosus, type I diabetes,
 CC rheumatoid arthritis, myasthenia gravis, multiple sclerosis, infectious
 CC diseases of the immune system (e.g. AIDS (acquired immunodeficiency
 CC syndrome)) and chronic immunosuppression. The present sequence is an
 CC immunotoxin fusion protein of the invention comprising 390 residues from
 CC the N-terminal glycine of mature DT toxin, a (Gly4Ser)3 linker and one
 CC single Fv chain from antibody UCHT1

SQ Sequence 637 AA;

Query Match 75.5%; Score 994; DB 5; Length 637;
 Best Local Similarity 78.0%; Pred. No. 7.1e-59;
 Matches 195; Conservative 13; Mismatches 34; Indels 8; Gaps 2;

QY 1 DIQMTQTSSLSASLGRVTVSCRASODIRNYLWYQKPDGVTKLIIYTSRLQGVPS 60
 DB 393 DIQMTQTSSLSASLGRVTVSCRASODIRNYLWYQKPDGVTKLIIYTSRLQGVPS 452
 QY 61 RFGSGSGGTGYSLTINLBOEDIGTVFCQGNTPMPTFGGCTKLEIKRGGSGSDGGSGSG 120
 DB 453 RFGSGSGGTGYSLTINLBOEDIGTVFCQGNTPMPTFGGCTKLEIKRGGSGSDGGSGSG 507
 QY 121 GSGSGSGSEVQLQSGPELVKPGASVKISCKDSGYAFNMMWVMVKRPGQGLEWIGRIY 180

Db 508 GSGSGGSEVQLQSGPELVKFGASMKISCKASGYSTFGYTMWVKQSHGKMLEWMLIN 567
 QY 181 PGDGSNNGKFEKRAILITADKSSSTAYWQLSLTVDSAVYFCARSGLL--RYANDYW 237
 Db 568 PYKGVSTYQKFKDRAITFDKSSSTAYWELLSTSEDSAVYVCARSGYGDSDWYFDW 627
 QY 238 GGGTSVTSS 247
 Db 628 GGGTTLTVFS 637

RESULT 7
 AAU75370
 ID AAU75370 standard; protein; 638 AA.

AC AAU75370;
 DT 23-APR-2002 (first entry)
 DE Diphtheria toxin/UCHT1 immunotoxin fusion protein #6.

KM Immunotoxin; pseudomonas exotoxin A; ETA; diphtheria toxin; DT;
 KM cytotoxic; immunosuppressive; immunostimulant; antidiabetic;
 KM antineumatic; antiarthritic; anti-HIV; anti-inflammatory;
 KM anti-T cell immunotoxin fusion protein; antibody; UCHT1;
 KM (GlySer)3 linker; T cell leukemia; lymphoma; graft-versus-host disease;
 KM systemic lupus erythematosus; transplant rejection;
 KM myasthenia gravis; multiple sclerosis; AIDS;
 KM acquired immunodeficiency syndrome; chronic immunosuppression.

OS Mus sp.
 OS Corynebacterium diphtheriae.
 OS Synthetic.
 OS Chimeric.

PN MO200187982-A2.

PD 22-NOV-2001.

PF 18-MAY-2001; 2001MO-US016125.

PR 18-MAY-2000; 2000US-00573797.

PA (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS-ERFINDUNGEN VERM GES MBH.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Neville DM, Thompson JT, Hu H, Woo J, Ma S, Hexham JM, Digan ME;
 DR WPI, 2002-121980/16.

PT New anti-T cell immunotoxin fusion protein comprising a truncated
 PT diphtheria toxin moiety, a connector, and one single chain Fv of the
 PT variable region of a UCHT1 antibody, useful for treating e.g. autoimmune
 PT diseases.

PS Claim 19; Page 269-270; 307pp; English.

XX The invention relates to an anti-T cell immunotoxin fusion protein,
 CC comprising from the amino terminus, a truncated diphtheria toxin moiety,
 CC a connector, and one single chain Fv of the variable region of a UCHT1
 CC antibody. The single chain Fv comprises VL, L, or VH. L is a Gly-Ser
 CC linker, and VL and VH are the variable light and heavy domains of the
 CC anti-CD3 antibody UCHT1. Also included are a nucleic acid encoding the
 CC novel immunotoxin fusion protein, a vector comprising the nucleic acid
 CC and a cell comprising the nucleic acid. The immunotoxin may also be a
 CC pseudomonas exotoxin A (ETA). The immunotoxins are useful for treating T
 CC cell leukemias or lymphomas, graft-versus-host diseases, and autoimmune
 CC diseases by inducing immune tolerance. The immunotoxin fusion proteins
 CC may be used in vivo to systemically reduce populations of T cells, or ex
 CC vivo to effect T-cell depletion from a treated cell population. The
 CC fusion proteins can be administered to a subject who is or will be a

CC recipient of an allotransplant to prevent or reduce T-cell mediated acute
 CC or chronic transplant rejection of the transplanted allogeneic cells,
 CC tissue or organ in the subject as well as treat other T-cell mediated
 CC diseases such as systemic lupus erythematosus, type I diabetes,
 CC rheumatoid arthritis, myasthenia gravis, multiple sclerosis, infectious
 CC diseases of the immune system (e.g. AIDS (acquired immunodeficiency
 CC syndrome)) and chronic immunosuppression. The present invention is an
 CC immunotoxin fusion protein of the invention comprising 390 residues from
 CC the N-terminal glycine of mature DT toxin, a (Gly4Ser)3 linker and one
 CC single Fv chain from antibody UCHT1
 CC XX

SQ Sequence 638 AA;

Query Match 75.5%; Score 994; DB 5; Length 638;

Best Local Similarity 78.0%; Pred. No. 7.1e-59; Matches 195; Conservative 13; Mismatches 34; Indels 8; Gaps 2;

QY 1 DIQWTQTSSLSASLGDRTVSCRAQDIRNYLNMVQKPDGTVKFLIYTSRLOGPVS 60
 Db 394 DIQWTQTSSLSASLGDRTVSCRAQDIRNYLNMVQKPDGTVKFLIYTSRLOGPVS 453
 QY 61 RFGSGSGCTVYSLTINNLBEDIGTYFCQCGNTPPMTFGCGTLEIKRGGGSDGSGSG 120
 Db 454 RFGSGSGCTVYSLTINNLBEDIGTYFCQCGNTLPMTFAGTLEIKRG---GGSGSG 508
 QY 121 GSGSGGSEVQLQSGPELVKFGASMKISCKASGYSTFGYTMWVKQSHGKMLEWMLIN 180
 Db 509 GSGSGGSEVQLQSGPELVKFGASMKISCKASGYSTFGYTMWVKQSHGKMLEWMLIN 568
 QY 181 PGDGSNNGKFEKRAILITADKSSSTAYWQLSLTVDSAVYFCARSGLL--RYANDYW 237
 Db 569 PYKGVSTYQKFKDRAITFDKSSSTAYWELLSTSEDSAVYVCARSGYGDSDWYFDW 628
 QY 238 GGGTSVTSS 247
 Db 629 GGGTTLTVFS 638

RESULT 8
 AAU75383

ID AAU75383 standard; protein; 656 AA.

AC AAU75383;

DT 23-APR-2002 (first entry)

DE Immunotoxin fusion protein related sequence #2.

XX Immunotoxin; pseudomonas exotoxin A; ETA; diphtheria toxin; DT;
 KM cytotoxic; immunosuppressive; immunostimulant; antidiabetic;
 KM antineumatic; antiarthritic; anti-HIV; anti-inflammatory;
 KM anti-T cell immunotoxin fusion protein; antibody; scUCHT1; Fv; CD3;
 KM T cell leukemia; lymphoma; graft-versus-host disease;
 KM autoimmune disease; transplant rejection; systemic lupus erythematosus;
 KM type I diabetes; rheumatoid arthritis; myasthenia gravis;
 KM multiple sclerosis; AIDS; acquired immunodeficiency syndrome;
 KM chronic immunosuppression.

OS Unidentified.

PN MO200187982-A2.

PD 22-NOV-2001.

PF 18-MAY-2001; 2001MO-US016125.

PR 18-MAY-2000; 2000US-00573797.

PA (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS-ERFINDUNGEN VERM GES MBH.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Neville DM, Thompson JT, Hu H, Woo J, Ma S, Hexham JM, Digan ME;

XX WPI; 2002-121980/16.
XX
XX New anti-T cell immunotoxin fusion protein comprising a truncated
PT diphtheria toxin moiety, a connector, and one single chain Fv of the
PT variable region of a UCHL1 antibody, useful for treating e.g. autoimmune
PT diseases.
XX
XX Disclosure; Page 282-283; 307pp; English.

XX The invention relates to an anti-T cell immunotoxin fusion protein,
XX comprising from the amino terminus, a truncated diphtheria toxin moiety,
XX a connector, and one single chain Fv of the variable region of a UCHL1
XX antibody. The single chain Fv comprises VL, L, or VH, L is a Gly-Ser
XX linker, and VL and VH are the variable light and heavy domains of the
XX anti-CD3 antibody UCHL1. Also included are a nucleic acid encoding the
XX novel immunotoxin fusion protein, a vector comprising the nucleic acid
XX and a cell comprising the nucleic acid. The immunotoxin may also be a
XX pseudomonas endotoxin A (ETA). The immunotoxins are useful for treating T
XX cell leukemias or lymphomas, graft-versus-host diseases, and autoimmune
XX diseases by inducing immune tolerance. The immunotoxin fusion proteins
XX may be used in vivo to systemically reduce populations of T cells, or ex
XX vivo to effect T-cell depletion from a treated cell population. The
XX fusion proteins can be administered to a subject who is or will be a
XX recipient of an allotransplant to prevent or reduce T-cell mediated acute
XX or chronic transplant rejection of the transplanted allogeneic cells,
XX tissue or organ in the subject as well as treat other T-cell mediated
XX diseases such as systemic lupus erythematosus, type I diabetes,
XX rheumatoid arthritis, myasthenia gravis, multiple sclerosis, infectious
XX diseases of the immune system (e.g. AIDS (acquired immunodeficiency
XX syndrome)) and chronic immunosuppression. The present sequence is a
XX protein sequence included in the sequence listing but not mentioned
XX elsewhere in the specification, associated with the immunotoxin fusion
XX proteins of the invention

XX Sequence 656 AA;

Query Match 75.5%; Score 994; DB 5; Length 656;
Best Local Similarity 78.0%; Pred. No. 7.3e-59;
Matches 195; Conservative 13; Mismatches 34; Indels 8; Gaps 2;

QY 1 DIQMTQTSSLSASLGRVTVSCASQDINRYLWYQKPDGTVKFLIYTSRLQPVPS 60
DB 412 DIQMTQTSSLSASLGRVTVSCASQDINRYLWYQKPDGTVKFLIYTSRLHSGVPS 471
QY 61 RFGSGSGGTDTYSLTINNLEOEDIGTVPCCQGNTPMTFGGTLLEIKRGGGSGSG 120
DB 472 KFGSGSGGTDTYSLTINNLEOEDIGTVPCCQGNTPMTFGGTLLEIKRGGGSGSG 526
QY 121 GSGSGSGSEVQLOQSGELVYKPGASVKISCKDGYANSSMMWVKORPGQGLFGRY 180
DB 527 GSGSGSGSEVQLOQSGELVYKPGASVKISCKDGYANSSMMWVKORPGQGLFGRY 186
QY 181 PGDDSNVNGFEGEKALITADKSSSTAYMOLSTVSDSAVYFCARSGLL--RYAMDY 237
DB 587 PYKVSRYNKKFKXKACFTYDKSSSTAYMOLSTVSDSAVYFCARSGVGDSDWFDW 646
QY 238 GQGTSTVYSS 247
DB 647 GQGTSTVYSS 656

RESULT 9
AAU75389 standard; protein; 657 AA.

XX 23-APR-2002 (first entry)
XX
XX Diphtheria toxin/UCHL1 immunotoxin fusion protein H18D1390-sfv.
XX

KM cytotatic; immunosuppressive; immunostimulant; antidiabetic;
KM antirheumatic; antiarthritic; anti-HIV; anti-inflammatory;
KM anti-T cell immunotoxin fusion protein; antibody; UCHL1;
KM (Gly4Ser)3 linker; T cell leukemia; lymphoma; graft-versus-host disease;
KM Fv; autoimmune disease; transplant rejection;
KM systemic lupus erythematosus; type I diabetes; rheumatoid arthritis;
KM myasthenia gravis; multiple sclerosis; AIDS; H18D1390-sfv;
KM acquired immunodeficiency syndrome; chronic immunosuppression.

XX Mus sp.
XX Corynebacterium diphtheriae.
XX Synthetic.
XX Chimeric.

XX WO200187982-A2.

XX 22-NOV-2001.

XX 18-MAY-2001; 2001WO-US016125.

XX 18-MAY-2000; 2000US-00573797.

XX (NOVS) NOVARTIS AG.
XX (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Neville DM, Thompson JT, Hu H, Moo J, Ma S, Hexham JM, Digan ME;
XX WPI; 2002-121980/16.

XX New anti-T cell immunotoxin fusion protein comprising a truncated
PT diphtheria toxin moiety, a connector, and one single chain Fv of the
PT variable region of a UCHL1 antibody, useful for treating e.g. autoimmune
PT diseases.

XX Example 30; Fig 34; 307pp; English.

XX The invention relates to an anti-T cell immunotoxin fusion protein,
XX comprising from the amino terminus, a truncated diphtheria toxin moiety,
XX a connector, and one single chain Fv of the variable region of a UCHL1
XX antibody. The single chain Fv comprises VL, L, or VH, L is a Gly-Ser
XX linker, and VL and VH are the variable light and heavy domains of the
XX anti-CD3 antibody UCHL1. Also included are a nucleic acid encoding the
XX novel immunotoxin fusion protein, a vector comprising the nucleic acid
XX and a cell comprising the nucleic acid. The immunotoxin may also be a
XX pseudomonas endotoxin A (ETA). The immunotoxins are useful for treating T
XX cell leukemias or lymphomas, graft-versus-host diseases, and autoimmune
XX diseases by inducing immune tolerance. The immunotoxin fusion proteins
XX may be used in vivo to systemically reduce populations of T cells, or ex
XX vivo to effect T-cell depletion from a treated cell population. The
XX fusion proteins can be administered to a subject who is or will be a
XX recipient of an allotransplant to prevent or reduce T-cell mediated acute
XX or chronic transplant rejection of the transplanted allogeneic cells,
XX tissue or organ in the subject as well as treat other T-cell mediated
XX diseases such as systemic lupus erythematosus, type I diabetes,
XX rheumatoid arthritis, myasthenia gravis, multiple sclerosis, infectious
XX diseases of the immune system (e.g. AIDS (acquired immunodeficiency
XX syndrome)) and chronic immunosuppression. The present sequence is an
XX immunotoxin fusion protein of the invention comprising 390 residues from
XX the N-terminal glycine of mature DT toxin, a linker and one single Fv
XX chain from antibody UCHL1, H18D1390-sfv

XX Sequence 657 AA;

Query Match 75.5%; Score 994; DB 5; Length 657;
Best Local Similarity 78.0%; Pred. No. 7.3e-59;
Matches 195; Conservative 13; Mismatches 34; Indels 8; Gaps 2;

QY 1 DIQMTQTSSLSASLGRVTVSCASQDINRYLWYQKPDGTVKFLIYTSRLQPVPS 60
DB 413 DIQMTQTSSLSASLGRVTVSCASQDINRYLWYQKPDGTVKFLIYTSRLHSGVPS 472

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DB 473 KFSGSGSDTDYSLTISNLEQEDIAIFYCQCGNTLPMWTFAGTKLEIKRG-----GGGSGG 527
QY 121 GSGGGGSEVQLQSGPELVKPGASVKISCKDGYAFPMSSMMNNVKORPGGLEWIGRIY 180
DB 528 GSGGGGSEVQLQSGPELVKPGASVKISCKDGYAFPMSSMMNNVKORPGGLEWIGRIY 587
QY 181 PGDGSNNGKFEKAILTADKSSSTAYVQLSLTSVDSAVYFCARSGLL---RYANDYW 237
DB 588 PYKGVSTNNGKFKDAXTLTVDKSSSTAYVQLSLTSVDSAVYFCARSGYDSDMYFDW 647
QY 238 GQGTSTVTVSS 247
DB 648 GQGTTLTVFS 657

RESULT 10
AB07461
ID AAB07461 standard; protein; 601 AA.
AC AAB07461;
XX 20-OCT-2000 (first entry)
DT
DE An immunotoxin comprising a CD3 binding domain and PE28.
XX
XX Immunotoxin; CD3-binding domain; Pseudomonas exotoxin A; immune system;
XX scFv (UCHT-1)-PE28; T-cell mediated disease; transplant rejection;
XX host versus graft disease; graft versus host disease;
XX bone marrow transplant.
XX
XX Synthetic.
XX Mus sp.
XX Pseudomonas aeruginosa.
OS
OS
FH Key Location/Qualifiers
FT Region 3..112
FT /note="variable region of the light chain"
FT 128..249
FT Region /note="variable region of the heavy chain"
XX
XX WO20041474-A2.
XX
XX 20-JUL-2000.
XX
XX 13-JAN-2000; 2000WO-BP000245.
XX
XX 15-JAN-1999; 99US-00234445.
XX PR 25-JAN-1999; 99US-00236968.
XX PR 07-OCT-1999; 99US-00414134.
XX
XX (NOV) NOVARTIS AG.
XX (NOV) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
XX Digan ME, Lake P, Wright RM;
XX
XX WPI; 2000-482739/42.
XX DR N-PSDB; AAA58773.
XX
XX Recombinant immunotoxin used for prophylaxis and treatment of T-cell
XX mediated diseases e.g. transplantation rejection.
XX
XX Claim 3; Page 60-63; 75pp; English.
XX
XX The present sequence represents a recombinant immunotoxin comprising a
XX CD3-binding domain and a Pseudomonas exotoxin A component. It is
XX designated scFv(UCHT-1)-PE28. The immunotoxins of the invention are used
XX for the prophylaxis or treatment of T-cell mediated diseases or
XX conditions of the immune system. They are also used to condition a
XX patient to be transplanted with cells, or a tissue or an organ of a donor
XX and for the prophylaxis and/or treatment of acute or chronic
XX transplantation rejection, host versus graft disease and/or graft versus
XX host disease in a patient to undergo a bone marrow transplant, where the

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CC CD3-bearing cell population in the patient is depleted and an inoculum
CC comprising isolated bone marrow and/or stem-cell enriched peripheral
CC blood cells of the donor treated with immunotoxin is inoculated into the
CC patient
XX
XX Sequence 601 AA:
SQ
QY 1 DIOMTTSLSASLDRVTVSCRAQSDIRNTLNNYQKPEPDGVKFLIYYTSRLQGVPS 60
DB 3 DIOMTTSLSASLDRVTVSCRAQSDIRNTLNNYQKPEPDGVKFLIYYTSRLSHGVPS 62
QY 61 RFGSGSGTDYSLTINLEQEDIGIFYCQCGNTLPMWTFAGTKLEIKRGCGGSDGGSGG 120
DB 63 KFSGSGSDTDYSLTISNLEQEDIAIFYCQCGNTLPMWTFAGTKLEIKRAGGS-GGGSGG 121
QY 121 GSGGGGSEVQLQSGPELVKPGASVKISCKDGYAFPMSSMMNNVKORPGGLEWIGRIY 180
DB 122 G--SGGSEVQLQSGPELVKPGASVKISCKDGYAFPMSSMMNNVKORPGGLEWIGRIY 179
QY 181 PGDGSNNGKFEKAILTADKSSSTAYVQLSLTSVDSAVYFCARSGLL---RYANDYW 237
DB 180 PYKGVSTNNGKFKDAXTLTVDKSSSTAYVQLSLTSVDSAVYFCARSGYDSDMYFDW 239
QY 238 GQGTSTVTVSS 247
DB 240 GAGTTLTVFS 249

RESULT 11
ABG72265
ID ABG72265 standard; protein; 601 AA.
AC ABG72265;
XX 06-MAR-2003 (first entry)
DT
DE Recombinant immunotoxin, scFv (UCHT-1)-PE38.
XX
XX Recombinant immunotoxin; scFv (UCHT-1)-PE38; single chain Fv fragment;
XX murine; anti-human CD3-monoclonal antibody binding domain; UCHT-1;
XX Pseudomonas aeruginosa; exotoxin A; ADP-ribosylating; translocation;
XX T-cell mediated disorder; organ transplantation rejection;
XX autoimmune disease; graft versus host disease; bone marrow transplant;
XX acquired immunodeficiency syndrome; AIDS; T-cell leukaemia;
XX T-cell lymphoma; T-cell-mediated autoimmune disease; type I diabetes;
XX systemic lupus erythematosus; rheumatoid arthritis; myasthenia gravis;
XX multiple sclerosis; immunological tolerance; osteoporosis;
XX aplastic anaemia; Gaucher's disease; thalassaemia; mutant; mutein.
XX
XX Mus sp.
XX Pseudomonas aeruginosa.
OS
OS Synthetic.
OS Chimeric.
XX
XX Key Location/Qualifiers
FH Region 3..111
FT /note="light chain variable region (VL)"
FT 112..127
FT Peptide /note="linker peptide (L)"
FT 128..249
FT Region /note="heavy chain variable region (VH)"
FT Peptide 250..254
FT /note="Connector peptide (C)"
FT 255..601
FT Region /note="PE38 mutant"
XX
XX US2002142000-A1.
XX
XX 03-OCT-2002.

```

XX PF 10-JAN-2000; 2000US-00480236.
 XX PR 10-JAN-2000; 2000US-00480236.
 XX PA (DIGA/) DIGAN M E.
 XX PA (LAKE/) LAKE P.
 XX PA (WRIGHT/) WRIGHT R M.
 XX PI Digan ME, Lake P, Wright RM;
 XX DR WPI; 2003-155935/15.
 XX DR N-PDSB; ABX14413.
 XX PT Novel recombinant immunotoxin polypeptide useful for treatment or
 PT prophylaxis of T-cell mediated disorders or organ transplantation
 PT rejection, comprises a CD3-binding domain and a pseudomonas exotoxin
 PT mutant.
 XX PS Claim 17; Fig 15; 58pp; English.
 XX CC The present invention relates to a novel recombinant immunotoxin,
 CC scFv(UCHT-1)-PE38, and the polynucleotide sequence encoding it. The
 CC recombinant immunotoxin comprising a single chain (sc) Fv fragment of
 CC murine anti-human CD3-monoclonal antibody (UCHT-1) binding domain fused
 CC to a Pseudomonas aeruginosa exotoxin A (PE38) mutant having ADP-
 CC ribosylating and translocation functions but substantially diminished
 CC cell-binding ability. The recombinant immunotoxin is useful for the
 CC treatment or prophylaxis of T-cell mediated disorders, organ
 CC transplantation rejection or autoimmune disease in a patient. For
 CC example, scFv(UCHT-1)-PE38 may be used for treatment or prophylaxis
 CC against graft versus host disease in a patient undergoing a bone marrow
 CC transplant, for the treatment or prophylaxis of transplant rejection in a
 CC patient to undergo a bone marrow transplant, or for conditioning a
 CC patient to be transplanted with cells, tissue or organ of a donor.
 CC scFv(UCHT-1)-PE38 is also useful for treating acquired immunodeficiency
 CC syndrome (AIDS), T-cell leukemias or lymphomas, T-cell mediated
 CC autoimmune disease such as systemic lupus erythematosus, type I diabetes,
 CC rheumatoid arthritis, myasthenia gravis, multiple sclerosis, for inducing
 CC immunological tolerance, and for treating diseases curable or treatable
 CC by bone marrow transplantation, including leukemias, osteoporosis,
 CC aplastic anaemia, Gaucher's disease, and thalassemia. The present
 CC sequence represents recombinant immunotoxin, scFv(UCHT-1)-PE38
 XX SQ Sequence 601 AA;

Query Match 75.3%; Score 992; DB 6; Length 601;
 Best Local Similarity 78.8%; Pred. No. 9,1e-59;
 Matches 197; Conservative 12; Mismatches 35; Indels 6; Gaps 3;

QY 1 DIQWOTTSLSASIGRWVNSCRASODIRNYNMYOQKRDGVVKEIYTSLSQGVNS 60
 DB 3 DIQWOTTSLSASIGRWVNSCRASODIRNYNMYOQKRDGVVKEIYTSLSQGVNS 62
 QY 61 RFGSGSGGTIVSLTINNLEQEDICTVPCQCGNTPTPMTFGGTYLKEIRGGSGSGSGG 120
 DB 63 KFGSGSGGTIVSLTINNLEQEDICTVPCQCGNTPTPMTFGGTYLKEIRAGGSGS 121
 QY 121 GSGSGSGSEVOLOOSGGEIVKPGASVYKISCKDSYANSSMMVMYORPCQGLEWIGRIY 180
 DB 122 G--SGGSEVQLQSGSELVKPGASVYKISCKDSYANSSMMVMYORPCQGLEWIGRIY 179
 QY 181 PGDDSYNNGKFEKKAIIITADKSSSTAYMOSSLTYSVDSAVYTCARSGLL--RYANDYV 237
 DB 180 PYKGVSTNOKFKOKATITVDKSSSTAYMEHLTISBDSAVYTCARSGYGDSDYFDVW 239
 QY 238 GCGTSYVWS 247
 DB 240 GAGTIVVSS 249

ID AAU75382 standard; protein; 642 AA.
 XX AC AAU75382;
 XX AC AAU75382;
 XX DT 23-APR-2002 (first entry)
 XX DE Diphtheria toxin/UCHT1 immunotoxin fusion protein DT389.sfv(UCHT1).
 XX XX
 XX KM Immunotoxin; pseudomonas exotoxin A; ETA; diphtheria toxin; DT;
 KM cytosolic; immunosuppressive; immunostimulant; antidiabetic;
 KM antineumatic; antiarthritic; anti-HIV; anti-inflammatory;
 KM anti-T cell immunotoxin fusion protein; antibody; UCHT1;
 KM (GlySer)3 linker; T cell leukaemia; lymphoma; graft-versus-host disease;
 KM Fv; autoimmune disease; transplant rejection;
 KM systemic lupus erythematosus; type I diabetes; rheumatoid arthritis;
 KM myasthenia gravis; multiple sclerosis; AIDS; DT389.sfv(UCHT1);
 KM acquired immunodeficiency syndrome; chronic immunosuppression.
 XX XX
 XX OS Mus sp.
 XX OS Corynebacterium diphtheriae.
 XX OS Synthetic.
 XX OS Chimeric.
 XX PN WO200187982-A2.
 XX PD 22-NOV-2001.
 XX PF 18-MAY-2001; 2001WO-US016125.
 XX PR 18-MAY-2000; 2000US-00573797.
 XX PA (NOVS) NOVARTIS AG.
 XX PA (NOVS) NOVARTIS-ERINDUNGEN VERN GRS MBH.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Neville DM, Thompson JT, Hu H, Moo J, Ma S, Hexham JM, Digan ME;
 XX WPI; 2002-121980/16.
 XX DR N-PDSB; ABX13467.
 XX DR
 XX PT New anti-T cell immunotoxin fusion protein comprising a truncated
 PT diphtheria toxin moiety, a connector, and one single chain Fv of the
 PT variable region of a UCHT1 antibody, useful for treating e.g. autoimmune
 PT diseases.
 XX PT
 XX PS Claim 5; Fig 35; 307pp; English.
 XX XX
 XX CC The invention relates to an anti-T cell immunotoxin fusion protein,
 CC comprising from the amino terminus, a truncated diphtheria toxin moiety,
 CC a connector, and one single chain Fv of the variable region of a UCHT1
 CC antibody. The single chain Fv comprises VL, L, or VH, L is a Gly-Ser
 CC linker and VL and VH are the variable light and heavy domains of the
 CC anti-CD3 antibody UCHT1. Also included are a nucleic acid encoding the
 CC novel immunotoxin fusion protein, a vector comprising the nucleic acid
 CC and a cell comprising the nucleic acid. The immunotoxin may also be a
 CC pseudomonas endotoxin A (ETA). The immunotoxins are useful for treating T
 CC cell leukemias or lymphomas, graft-versus-host diseases, and autoimmune
 CC diseases by inducing immune tolerance. The immunotoxin fusion proteins
 CC may be used in vivo to systematically reduce populations of T cells, or ex
 CC vivo to effect T-cell depletion from a treated cell population. The
 CC fusion proteins can be administered to a subject who is or will be a
 CC recipient of an allograft or transplant to prevent or reduce T-cell mediated acute
 CC or chronic transplant rejection of the transplanted allogeneic cells,
 CC tissue or organ in the subject as well as treat other T-cell mediated
 CC diseases such as systemic lupus erythematosus, type I diabetes,
 CC rheumatoid arthritis, myasthenia gravis, multiple sclerosis, infectious
 CC diseases of the immune system (e.g. AIDS (acquired immunodeficiency
 CC syndrome) and chronic immunosuppression. The present sequence is an
 CC immunotoxin fusion protein of the invention comprising 369 residues from
 CC the N-terminal glycine of mature DT toxin, a (GlySer)3 linker and one
 CC single Fv chain from antibody UCHT1, DT389.sfv(UCHT1)
 XX SQ Sequence 642 AA;

Thu Apr 22 14:51:00 2004

us-10-620-049-23.rag

Page 11

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Query Match: 75.3%; Score 992; DB 5; Length 642;
Best Local Similarity 78.8%; Pred. No. 9.7e-59;
Matches 197; Conservative 12; Mismatches 35; Indels 6; Gaps 3

QY      1 DDMTQTSSLSASLGDRTVSCRASODIRNYLAMYQKXPBGTYKFLIYTSRLQGVGS 60
DB      396 DDMQTTSLSLSLSDRVLTSICRASODIRNYLAMYQKXPBGTYKLLIYTSRLHSGVGS 455
QY      61 RFGSGSGSDYSLTINLLEQEDIGTYFCQOQNTPTPTFGGCTKLEIRRGGSGSDGGGSG 120
DB      456 KFGSGSGSDTYSLTINLLEQEDIAATYFCQOQNTLPTPTAGTKEIRRAGGGS-GGSSGG 514
QY      121 GSGSGSGSSEYQLQOQSGPELVKPGASVYKISCHDSGIAFPHSSMMNMYKVRPQGLENGRLY 180
DB      515 G--SGGSGSEYQLQOQSGPELVKPGASVKISCKRSGSGSPGTMMNMYKSHGNNLEHMLLN 572
QY      181 PGDGDSDNYNKGFEFGKAILTPADKSSSTAYWQLSSLTSDVASAYFYCARSGLL--RYANDY 237
DB      573 PYKGVSTYNNKFPDKKATLTFYDKSSSTAYWELLSTSDSDASAYFYCARSGYGDSDPWFYDW 632
QY      238 GQGSYTVVSS 247
DB      633 GAGTIVTVSS 642

```

RESULT 13

ID AA029675 standard; protein; 642 AA.

AC	AA029675;	
XX		
DT	22-SEP-2003	(first entry)
XX		
DE	Anti-T cell immunotoxin fusion protein #6	

KM Immunotoxin; anti-T-cell, fusion protein, chemotherapeutic agent;
 KM diphtheria toxin; Pseudomonas toxin; proliferative disease;
 KM T-cell leukaemia; T-cell lymphoma; T-cell granular lymphatic leukaemia;
 KM aggressive natural killer cell leukaemia; hairy-cell leukaemia;
 KM Seary syndrome; angioimmunoblastic T-cell lymphoma;
 KM cutaneous T-cell lymphoma.
 XX
 OS Unidentified.

Unidentified.

PN	MO2003045429-A2.
PD	05-JUN-2003.
PE	27-NOV-2002; 2002MO-EP013387
PF	28-NOV-2001; 2001GB-00028510
PG	(NOVS) NOVARTIS AG.
PH	(NOVS) NOVARTIS PHARMA GMBH
PI	

XX	Engel G;
PI	
XX	
DR	WPI; 2003-432489/45.
XX	
PT	Combination for treating malignant proliferative disease, e.g. leukemia
PT	and lymphoma, has an anti-T cell immunotoxin fusion protein comprising a
PT	diphtheria/pseudomonas toxin and a targeting moiety, and a
PT	chemotherapeutic agent.

PS Claim 7; Page 55-59; 66pp; English.

CC The invention relates to a novel combination comprising an anti-T cell
CC immunotoxin fusion protein and at least one chemotherapeutic agent. The
CC fusion protein comprises a diphtheria or Pseudomonas toxin moiety and a
CC targeting moiety suitable for targeting the fusion protein to T cells.
CC The novel combination is useful for preparing pharmaceutical compositions
CC that is useful for delaying the progression of or for the treatment of a

CC Subject, in particular T-cell leukaemia, T-cell lymphoma, including T-
CC cell, malignant proliferative disease such as lymphoma or leukaemia in a
CC subject, in particular T-cell leukaemia, T-cell lymphoma, including T-
CC cell, granular lymphatic leukaemia, aggressive natural killer cell
CC leukaemia, hairy-cell leukaemia, Sezary syndrome, angioimmunoblastic T-
CC cell lymphoma, peripheral T-cell lymphoma unspecified, cutaneous T-cell
CC lymphoma, subcutaneous panniculitis like T-cell lymphoma, and
CC hepatosplenic gamma/delta T-cell lymphoma. The present sequence is an
CC example of anti-T cell immunotoxin fusion protein of the invention
XX
SQ Sequence 642 AA;

Query Match	Score	DB	Length
75.38;	992;	6;	6427

RESULT 14

ID AU75390 standard; protein; 643 AA.

AAU75390;
23-APR-2002 (first entry)

DE Diphtheria toxin/UCHT1 immunotoxin fusion protein DT389.scrv(UCHT1).
XX
KM Immunotoxin; pseudomomas exotoxin A; ETA; diphtheria toxin; DT;
KM cyclostatin; immunosuppressive; immunostimulant; antidiabetic;
KM antirheumatic; antiarthritic; anti-HIV; anti-inflammatory;
KM anti-T cell immunotoxin fusion protein; antibody; UCHT1;
KM (Gly36Sr) linker; T cell leukemia; lymphoma; graft-versus-host disease;
KM Fv; autoimmune disease; transplant rejection;
KM systemic lupus erythematosus; type I diabetes; rheumatoid arthritis;
KM myasthenia gravis; multiple sclerosis; AIDS; DT389.scrv(UCHT1);
KM acquired immunodeficiency syndrome; chronic immunosuppression.

OS	Mus sp.
OS	<i>Corynebacterium diphtheriae</i>
OS	Synthetic.
OS	Chimeric.

PN WO200187982-A2.

PD 22-NOV-2001

PF 18-MAY-2001; 2001WO-US016125.

PR 18-MAY-2000; .2000US-00573797.

PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Neville DM, Thompson JT, Hu H, Woo J, Ma S, Hexham JM, Digan ME;
 XX WPI; 2002-121980/16.
 XX
 XX New anti-T cell immunotoxin fusion protein comprising a truncated
 PT diphtheria toxin moiety, a connector, and one single chain Fv of the
 PT variable region of a UCHL1 antibody, useful for treating e.g. autoimmune
 PT diseases.
 XX
 XX Claim 7; Fig 34; 307pp; English.

XX The invention relates to an anti-T cell immunotoxin fusion protein,
 CC comprising from the amino terminus, a truncated diphtheria toxin moiety,
 CC a connector, and one single chain Fv of the variable region of a UCHL1
 CC antibody. The single chain Fv comprises VL, L, or VH, L is a Gly-Ser
 CC linker, and VL and VH are the variable light and heavy domains of the
 CC anti-CD3 antibody UCHL1. Also included are a nucleic acid encoding the
 CC novel immunotoxin fusion protein, a vector comprising the nucleic acid
 CC and a cell comprising the nucleic acid. The immunotoxin may also be a
 CC pseudomonas endotoxin A (ETA). The immunotoxins are useful for treating T
 CC cell leukaemias or lymphomas, graft-versus-host diseases, and autoimmune
 CC diseases by inducing immune tolerance. The immunotoxin fusion proteins
 CC may be used in vivo to systemically reduce populations of T cells, or ex
 CC vivo to effect T-cell depletion from a treated cell population. The
 CC fusion proteins can be administered to a subject who is or will be a
 CC recipient of an allotransplant to prevent or reduce T-cell mediated acute
 CC or chronic transplant rejection of the transplanted allogeneic cells,
 CC tissue or organ in the subject as well as treat other T-cell mediated
 CC diseases such as systemic lupus erythematosus, type I diabetes,
 CC rheumatoid arthritis, myasthenia gravis, multiple sclerosis, infectious
 CC diseases of the immune system (e.g. AIDS (acquired immunodeficiency
 CC syndrome)) and chronic immunosuppression. The present sequence is an
 CC immunotoxin fusion protein of the invention comprising 389 residues from
 CC the N-terminal glycine of mature DT toxin, a (Gly48Ser)3 linker and one
 CC single Fv chain from antibody UCHL1, DT389.scfv(UCHL1)
 CC
 XX Sequence 643 AA;

Query Match 75.3%; Score 992; DB 5; Length 643;
 Best Local Similarity 78.8%; Pred. No. 9.8e-59;
 Matches 197; Conservative 12; Mismatches 35; Indels 6; Gaps 3;

DB 1 DIQMTQTSSLSASLSDGRTVSCRASQDIRNYLMWYQKPDGTVKFLIYTSRLQGVPS 60
 DB 397 DIQMTQTSSLSASLSDGRTVSCRASQDIRNYLMWYQKPDGTVKFLIYTSRLHSGVPS 456
 QY 61 RFGSGSGGTGYSLTNNLEQEDIGTVFCQCGNTPEMTFGGTTKEIRKGGSGSGGGSGG 120
 DB 457 KFGSGSGGTGYSLTNNLEQEDIGTVFCQCGNTPEMTFGGTTKEIRKGGSGSGGGSGG 515
 QY 121 GSGSGSGSEVQLQSGPELVKPGASVKISCKDGYAFNSMMWVVKRPGQGLEMTGRIV 180
 DB 516 G--SGGSGSEVQLQSGPELVKPGASVKISCKASGYSTFGYTMWVVKSHGNLMMGLIN 573
 QY 181 PGDDSNYNGKPEKALITADKSSSTAYMQLSSITVDSAVYFCARSGLL--RYADWY 237
 DB 574 PYKGVSTYNQKPKKATLVDKSSSTAYMQLSSITVDSAVYFCARSGYGDSDWYFDWV 633
 QY 238 GQGTSTVTVSS 247
 DB 634 GAGTTVTVSS 643

RESULT 15
 ID AAO29670 standard; protein; 643 AA.
 XX AAO29670;
 XX AAO29670;
 XX 22-SEP-2003 (first entry)
 DE Anti-T cell immunotoxin fusion protein #1.

KW Immunotoxin; anti-T cell; fusion protein; chemotherapeutic agent;
 KW diphtheria toxin; Pseudomonas toxin; proliferative disease;
 KW T-cell leukaemia; T-cell lymphoma; T-cell granular lymphatic leukaemia;
 KW aggressive natural killer cell leukaemia; hairy-cell leukaemia;
 KW Sezary syndrome; angioimmunoblastic T-cell lymphoma;
 KW cutaneous T-cell lymphoma.
 XX
 XX Unidentified.
 XX
 XX WO2003045429-A2.
 XX
 XX 05-JUN-2003.
 XX
 XX 27-NOV-2002; 2002WO-BP013387.
 XX
 XX 28-NOV-2001; 2001GB-00028510.
 XX
 XX (NOVS) NOVARTIS AG.
 XX (NOVS) NOVARTIS PHARMA GMBH.
 XX
 XX Engel G;
 XX
 XX WPI; 2003-482489/45.
 XX
 XX Combination for treating malignant proliferative disease, e.g. leukemia
 PT and lymphoma, has an anti-T cell immunotoxin fusion protein comprising a
 PT diphtheria/Pseudomonas toxin and a targeting moiety, and a
 PT chemotherapeutic agent.
 PT
 PS Claim 7; Page 23-27; 66pp; English.

XX The invention relates to a novel combination comprising an anti-T cell
 CC immunotoxin fusion protein and at least one chemotherapeutic agent. The
 CC fusion protein comprises a diphtheria or Pseudomonas toxin moiety and a
 CC targeting moiety suitable for targeting the fusion protein to T cells.
 CC The novel combination is useful for preparing pharmaceutical composition
 CC that is useful for delaying the progression of or for the treatment of a
 CC malignant proliferative disease such as lymphoma or leukaemia in a
 CC subject, in particular T-cell leukaemia, T-cell lymphoma, including T-
 CC cell granular lymphatic leukaemia, aggressive natural killer cell
 CC leukaemia, hairy-cell leukaemia, Sezary syndrome, angioimmunoblastic T-
 CC cell lymphoma, peripheral T-cell lymphoma unspecified, cutaneous T-cell
 CC lymphoma, subcutaneous panniculitis like T-cell lymphoma, and
 CC hepatoplenic gamma/delta T-cell lymphoma. The present sequence is an
 CC example of anti-T cell immunotoxin fusion protein of the invention
 CC
 XX Sequence 643 AA;

Query Match 75.3%; Score 992; DB 5; Length 643;
 Best Local Similarity 78.8%; Pred. No. 9.8e-59;
 Matches 197; Conservative 12; Mismatches 35; Indels 6; Gaps 3;

DB 1 DIQMTQTSSLSASLSDGRTVSCRASQDIRNYLMWYQKPDGTVKFLIYTSRLQGVPS 60
 DB 397 DIQMTQTSSLSASLSDGRTVSCRASQDIRNYLMWYQKPDGTVKFLIYTSRLHSGVPS 456
 QY 61 RFGSGSGGTGYSLTNNLEQEDIGTVFCQCGNTPEMTFGGTTKEIRKGGSGSGGGSGG 120
 DB 457 KFGSGSGGTGYSLTNNLEQEDIGTVFCQCGNTPEMTFGGTTKEIRKGGSGSGGGSGG 515
 QY 121 GSGSGSGSEVQLQSGPELVKPGASVKISCKDGYAFNSMMWVVKRPGQGLEMTGRIV 180
 DB 516 G--SGGSGSEVQLQSGPELVKPGASVKISCKASGYSTFGYTMWVVKSHGNLMMGLIN 573
 QY 181 PGDDSNYNGKPEKALITADKSSSTAYMQLSSITVDSAVYFCARSGLL--RYADWY 237
 DB 574 PYKGVSTYNQKPKKATLVDKSSSTAYMQLSSITVDSAVYFCARSGYGDSDWYFDWV 633
 QY 238 GQGTSTVTVSS 247
 DB 634 GAGTTVTVSS 643

Thu Apr 22 14:51:00 2004

Search completed: April 22, 2004, 11:54:34
Job time : 53 secs

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OM protein - protein search, using sw model

Run on: April 22, 2004, 11:48:48 ; Search time 10.5 Seconds
(without alignments)
1224.888 Million cell updates/sec

Title: US-10-620-049-25

Perfect score: 1316

Sequence: 1 DIOMTQTSSLSASIGDRVT.....GLIRYANDYMGQGTSTVSS 247

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	508	38.6	108	1	KVSK_MOUSE
2	507	38.5	108	1	KVSN_MOUSE
3	506	38.4	108	1	KVSL_MOUSE
4	498	37.8	108	1	KVSM_MOUSE
5	494	37.5	108	1	KVSV_MOUSE
6	473	35.9	108	1	KVSV_MOUSE
7	454	34.5	108	1	KVSV_MOUSE
8	443	33.7	140	1	HV02_MOUSE
9	440.5	33.5	139	1	HV07_MOUSE
10	430	32.7	120	1	HV03_MOUSE
11	426.5	32.1	117	1	HV01_MOUSE
12	423	32.0	117	1	HV06_MOUSE
13	421	31.8	117	1	HV06_MOUSE
14	419	31.8	118	1	HV06_MOUSE
15	415	31.5	117	1	HV13_MOUSE
16	414	31.5	121	1	HV01_MOUSE
17	413	31.4	117	1	HV12_MOUSE
18	406.5	30.9	118	1	HV05_MOUSE
19	405	30.8	117	1	HV05_MOUSE
20	403	30.6	117	1	HV04_MOUSE
21	400.5	30.4	120	1	HV05_MOUSE
22	395	30.0	108	1	KVSP_MOUSE
23	389	29.6	108	1	KV1Y_HUMAN
24	388	29.5	117	1	HV09_MOUSE
25	388	29.5	130	1	KVSG_MOUSE
26	382	29.0	117	1	HV49_MOUSE
27	379	28.8	108	1	KV1B_HUMAN
28	379	28.8	108	1	KV10_HUMAN
29	378	28.8	117	1	HV10_MOUSE
30	378	28.7	108	1	KV1A_HUMAN
31	377	28.6	117	1	HV14_MOUSE
32	376	28.6	108	1	KV1P_MOUSE
33	376	28.6	108	1	KV1P_HUMAN

34	366	27.8	108	1	KV1H_HUMAN
35	366	27.8	108	1	KV1E_HUMAN
36	365	27.7	108	1	KV1E_HUMAN
37	365	27.7	128	1	KV1E_MOUSE
38	365	27.7	129	1	KV1E_MOUSE
39	364	27.7	108	1	KV1M_HUMAN
40	364	27.7	108	1	KV1Q_HUMAN
41	362	27.5	136	1	HV15_MOUSE
42	361	27.4	108	1	KV1C_HUMAN
43	361	27.4	108	1	KV1V_HUMAN
44	360	27.4	108	1	KV1G_HUMAN
45	356.5	27.1	147	1	HV1C_HUMAN

ALIGNMENTS

RESULT 1

ID KVSK_MOUSE STANDARD; PRT; 108 AA.

AC P01644; 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Ig kappa chain V-V region HP R16.7.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE.

RC STRAIN=AJ/;

RX MEDLINE=82150934; PubMed=6801658;

RA Stigleman W.; Capra J.D.; "Complete amino acid sequence of 18ht chain variable regions derived

RT from five monoclonal anti-p-azophenylarsenate antibodies differing

RL with respect to a crossreactive idiotype."

RT Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).

CC -1- MISCELLANEOUS: Anti-arsenate hybridoma protein.

DR PIR; A01927; KIMSAR.

DR HSRF; P01607; IREI.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_V.

DR Pfam; PF00047; Ig_V.

DR SMART; SMO0406; IGV; 1.

DR PROSITE; PS00835; IG_LIKE; 1.

ID KVEN MOUSE STANDARD; PRT; 108 AA.
 AC P01647;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ig kappa chain V-V region HP 12481.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RX MEDLINE=82150934; PubMed=6801658;
 RA Siegelman M., Capra J.D.;
 RT "Complete amino acid sequence of light chain variable regions derived from five monoclonal anti-p-azophenylarsenate antibodies differing with respect to a crossreactive idioType."
 RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
 CC -1- MISCELLANEOUS: Anti-arsenate hybridoma protein.
 DR HSSP; P01607; 1REI.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG-LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 3 50 FRAMEWORK-2.
 FT DOMAIN 4 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 5 57 FRAMEWORK-3.
 FT DOMAIN 6 88 FRAMEWORK-4.
 FT DISULFID 98 108 BY SIMILARITY.
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11965 MW; 399718C653EF58E CRC64;
 Query Match 38.5%; Score 507; DB 1; Length 108;
 Best Local Similarity 90.7%; Pred. No. 8.1e-33;
 Matches 98; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
 DB 1 DIOMQTSSLSASISGDRVTSCRASQDIPRYLWYQKPGDTYKFLIYYTSRLPGVPS 60
 1 DIOMQTSSLSASISGDRVTSCRASQDIPRYLWYQKPGDTYKFLIYYTSRLPGVPS 60
 61 RFSGSGSGTDYSLTINLEQEDIGTYFCQCGNTPEPTFGGKLEIKR 108
 61 RFSGSGSGTDYSLTINLEQEDIGTYFCQCGNTPEPTFGGKLEIKR 108
 DB 61 RFSGSGSGTDYSLTINLEQEDIGTYFCQCGNTPEPTFGGKLEIKR 108
 61 RFSGSGSGTDYSLTINLEQEDIGTYFCQCGNTPEPTFGGKLEIKR 108
 RESULT 3
 KVSJL_MOUSE STANDARD; PRT; 108 AA.
 ID KVSJL_MOUSE
 AC P01645;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ig kappa chain V-V region HP 93G7.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RX MEDLINE=82150934; PubMed=6801658;
 RA Siegelman M., Capra J.D.;
 RT "Complete amino acid sequence of light chain variable regions derived from five monoclonal anti-p-azophenylarsenate antibodies differing with respect to a crossreactive idioType."
 RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
 CC -1- MISCELLANEOUS: Anti-arsenate hybridoma protein.
 DR HSSP; P01607; 1REI.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG-LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 3 50 FRAMEWORK-2.
 FT DOMAIN 4 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 5 57 FRAMEWORK-3.
 FT DOMAIN 6 88 FRAMEWORK-4.
 FT DISULFID 98 108 BY SIMILARITY.
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11961 MW; D528DA5E9A45291C CRC64;
 Query Match 37.8%; Score 498; DB 1; Length 108;
 Best Local Similarity 88.9%; Pred. No. 4e-32;

DR HSSP; P01607; 1REI.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG-LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 3 50 FRAMEWORK-2.
 FT DOMAIN 4 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 5 57 FRAMEWORK-3.
 FT DOMAIN 6 88 FRAMEWORK-4.
 FT DISULFID 98 108 BY SIMILARITY.
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11954 MW; 22F4642C63EF58E CRC64;
 Query Match 38.4%; Score 506; DB 1; Length 108;
 Best Local Similarity 90.7%; Pred. No. 9.7e-33;
 Matches 98; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
 DB 1 DIOMQTSSLSASISGDRVTSCRASQDIPRYLWYQKPGDTYKFLIYYTSRLPGVPS 60
 1 DIOMQTSSLSASISGDRVTSCRASQDIPRYLWYQKPGDTYKFLIYYTSRLPGVPS 60
 61 RFSGSGSGTDYSLTINLEQEDIGTYFCQCGNTPEPTFGGKLEIKR 108
 61 RFSGSGSGTDYSLTINLEQEDIGTYFCQCGNTPEPTFGGKLEIKR 108
 DB 61 RFSGSGSGTDYSLTINLEQEDIGTYFCQCGNTPEPTFGGKLEIKR 108
 61 RFSGSGSGTDYSLTINLEQEDIGTYFCQCGNTPEPTFGGKLEIKR 108
 RESULT 4
 KVSQ_MOUSE STANDARD; PRT; 108 AA.
 ID KVSQ_MOUSE
 AC P01648;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ig kappa chain V-V region HP 91A3.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RX MEDLINE=82150934; PubMed=6801658;
 RA Siegelman M., Capra J.D.;
 RT "Complete amino acid sequence of light chain variable regions derived from five monoclonal anti-p-azophenylarsenate antibodies differing with respect to a crossreactive idioType."
 RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
 CC -1- MISCELLANEOUS: Anti-arsenate hybridoma protein.
 DR HSSP; P01607; 1REI.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG-LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 3 50 FRAMEWORK-2.
 FT DOMAIN 4 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 5 57 FRAMEWORK-3.
 FT DOMAIN 6 88 FRAMEWORK-4.
 FT DISULFID 98 108 BY SIMILARITY.
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11961 MW; D528DA5E9A45291C CRC64;
 Query Match 37.8%; Score 498; DB 1; Length 108;
 Best Local Similarity 88.9%; Pred. No. 4e-32;

Matches 96; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIOMTQTSSLSASLGRTVSCRASODIRNYLWYQKPDGTVKFLIYTSRLPGVPS 60
 DB 1 DIOMTQTSSLSASLGRTVSCRASODIRNYLWYQKPDGTVKFLIYTSRLPGVPS 60
 QY 61 RFSGSGGSDYSLTINNLEQEDIGTYPCQCGNTPTPFGGCTKLEIKR 108
 DB 61 RFSGSGGSDYSLTINNLEQEDIGTYPCQCGNTPTPFGGCTKLEIKR 108

RESULT 5

KVSM_MOUSE STANDARD; PRT; 108 AA.
 AC P01646;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE IG kappa chain V-V region HP 123B6.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=A/J;
 RX MEDLINE=62150934; PubMed=6801658;
 RA Siegelman M., Capra J.D.;
 RT "Complete amino acid sequence of light chain variable regions derived
 from five monoclonal anti-p-azophenylarsenate antibodies differing
 with respect to a crossreactive idiotype.";
 RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683 (1981).
 CC -1- MISCELLANEOUS: Anti-arsenate hybridoma protein.
 DR HSP; P01607; IREI.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00406; IG_1.
 DR PROSITE; PS50835; IG LIKE; 1.
 DR KX Immunoglobulin V region.

FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 98 108 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11989 MW; 4C98599C08BBA09A CRC64;

Query Match 37.5%; Score 494; DB 1; Length 108;
 Best Local Similarity 88.9%; Pred. No. 8.2e-32;
 Matches 96; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIOMTQTSSLSASLGRTVSCRASODIRNYLWYQKPDGTVKFLIYTSRLPGVPS 60
 DB 1 DIOMTQTSSLSASLGRTVSCRASODIRNYLWYQKPDGTVKFLIYTSRLPGVPS 60
 QY 61 RFSGSGGSDYSLTINNLEQEDIGTYPCQCGNTPTPFGGCTKLEIKR 108
 DB 61 RFSGSGGSDYSLTINNLEQEDIGTYPCQCGNTPTPFGGCTKLEIKR 108

RESULT 6

KVSM_MOUSE STANDARD; PRT; 108 AA.
 AC P04946;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG kappa chain V-V region NQ5-89.4.
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83271467; PubMed=6877353;
 RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
 RT "mRNA sequences define an unusually restricted IgG response to 2-
 phenylloxazoline and its early diversification.";
 RL Nature 304:320-324 (1983).
 CC -1- MISCELLANEOUS: ANTI-2-PHENYL OXAZOLONE (PROX) ANTIBODY.
 CC -----
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DR EMBL; K00745; AA38690.1; -.
 DR HSP; P01607; IREI.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00406; IG_1.
 DR PROSITE; PS50835; IG LIKE; 1.
 DR KX Immunoglobulin V region; Hybridoma.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 98 107 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11866 MW; DB2C885920DC6DD CRC64;

Query Match 35.9%; Score 473; DB 1; Length 108;
 Best Local Similarity 84.3%; Pred. No. 3.4e-30;
 Matches 91; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIOMTQTSSLSASLGRTVSCRASODIRNYLWYQKPDGTVKFLIYTSRLPGVPS 60
 DB 1 DIOMTQTSSLSASLGRTVSCRASODIRNYLWYQKPDGTVKFLIYTSRLPGVPS 60
 QY 61 RFSGSGGSDYSLTINNLEQEDIGTYPCQCGNTPTPFGGCTKLEIKR 108
 DB 61 RFSGSGGSDYSLTINNLEQEDIGTYPCQCGNTPTPFGGCTKLEIKR 108

Query Match 35.9%; Score 473; DB 1; Length 108;
 Best Local Similarity 84.3%; Pred. No. 3.4e-30;
 Matches 91; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIOMTQTSSLSASLGRTVSCRASODIRNYLWYQKPDGTVKFLIYTSRLPGVPS 60
 DB 1 DIOMTQTSSLSASLGRTVSCRASODIRNYLWYQKPDGTVKFLIYTSRLPGVPS 60
 QY 61 RFSGSGGSDYSLTINNLEQEDIGTYPCQCGNTPTPFGGCTKLEIKR 108
 DB 61 RFSGSGGSDYSLTINNLEQEDIGTYPCQCGNTPTPFGGCTKLEIKR 108

RESULT 7

KVSM_MOUSE STANDARD; PRT; 108 AA.
 AC P01643;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG kappa chain V-V region MOPC 173.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=76091934; PubMed=812696;
 RA Schiff C., Fougereau M.;
 RT "Determination of the primary structure of a mouse IgG2a
 immunoglobulin. Amino-acid sequence of the light chain.";
 RL Eur. J. Biochem. 59:525-537 (1975).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
 DR PIR; A01926; KMS73.

DR HSSP; P01607; 1RE1.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOWAIN 24 34 FRAMEWORK-1.
 FT DOWAIN 35 49 FRAMEWORK-2.
 FT DOWAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOWAIN 57 88 FRAMEWORK-3.
 FT DOWAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DOWAIN 98 108 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON TER 108
 SQ SEQUENCE 108 AA; 11819 MM; 2AD23D92A72AA0A3 CRC64;

Query Match 34.5%; Score 454; DB 1; Length 108;
 Best Local Similarity 79.6%; Pred. No. 1e-28;
 Matches 86; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIQVOTSSLSASIGDVTVCASODIRNYLNMWQKPDGVKFLIYTSRLPGVPS 60
 DB 1 DIQVOTSSLSASIGDVTVCASODIRNYLNMWQKPDGVKFLIYTSRLPGVPS 60
 QY 61 RFGSGSGTGYSLTINLEQEDIGTFYFCQGNTPMTFGGTXLEIKR 108
 DB 61 RFGSGSGTGYSLTINLEQEDIGTFYFCQGNTPMTFGGTXLEIKR 108

RESULT 8
 ID HV02_MOUSE STANDARD; PRT; 140 AA.
 AC P01746;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region 9367 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 NC NCB1_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A/J;
 RX MEDLINE=82152818; PubMed=6801765; Slaughter C., Tucker P.W.,
 RA Sims V., Rabbits T.H., Estes P., Slaughter C., Tucker P.W.,
 RA Capra J.D.;
 RT "Somatic mutation in genes for the variable portion of the
 immunoglobulin heavy chain.";
 RL Science 216:309-311(1982).
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
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 CC EMBL; J00493; AAA38128.1; -
 DR PIR; A94264; HVMG57.
 DR HSSP; P01810; 2FBJ.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; Hybridoma; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 140 IG HEAVY CHAIN V REGION 9367.

FT DOMAIN 20 139 IG-LIKE.
 FT NON TER 140
 SQ SEQUENCE 140 AA; 15514 MM; 25A4CBBE31DA5CE8 CRC64;

Query Match 33.7%; Score 443; DB 1; Length 140;
 Best Local Similarity 70.9%; Pred. No. 9.6e-28;
 Matches 90; Conservative 8; Mismatches 27; Indels 2; Gaps 1;

QY 123 SCGGSEVLOQSGELVYKPGASVXISCKDSGYAFNSSMMWVYKORPGGLEWIGRIYPG 182
 DB 14 TGVHSEVLOQSGELVYKPGASVXISCKDSGYAFNSSMMWVYKORPGGLEWIGRIYPG 73
 QY 183 DGDSTNGKFBGKAILTADKSSSTYVQSLTSDVSAVYFCARSGLL--RYANDYWGQ 240
 DB 74 NGYINYNKFKGKTYLTVDKSSSTYVQSLTSDVSAVYFCARSHYGGSDYDFYWGQ 133
 QY 241 TSVTVSS 247
 DB 134 TPLTVSS 140

RESULT 9
 ID HV07_MOUSE STANDARD; PRT; 139 AA.
 AC P01751; P01752;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region B1-8/186-2 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCB1_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RX MEDLINE=81234548; PubMed=6788376;
 RA Bothwell A.L.M., Paskind M., Rath M., Imanishi-Kari T., Rajewsky K.,
 RA Baltimore D.;
 RT "Heavy chain variable region contribution to the NPB family of
 antibodies: somatic mutation evident in a gamma 2a variable region.";
 RL Cell 24:625-637(1981).
 CC -1- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
 MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
 (NPB ANTIBODIES).
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 or send an email to license@sib-sib.ch).
 CC EMBL; J00529; AAA38170.1; -
 DR PIR; A90809; MEMS18.
 DR PDB; 1A6W; 27-MAY-98.
 DR PDB; 1A6W; 15-JUL-98.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; Signal; 3D-structure.
 FT SIGNAL 1 19
 FT CHAIN 20 139 IG HEAVY CHAIN V REGION B1-8/186-2.
 FT DOWAIN 20 49 FRAMEWORK-1.
 FT DOWAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOWAIN 55 68 FRAMEWORK-2.
 FT DOWAIN 69 85 FRAMEWORK-3.
 FT DOWAIN 86 117 COMPLEMENTARITY-DETERMINING-2.
 FT DOWAIN 118 124 FRAMEWORK-4.
 FT DOWAIN 125 139 D SEGMENT.
 FT CHAIN 125 139 JH2 SEGMENT.

Thu Apr 22 14:51:04 2004

US-10-620-049-25.TSP

Page 5

PT DISULFID 41 115 BY SIMILARITY.
FT NON TER 139 139
SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FDC9F465 CRC64;

Query Match 33.5%; Score 440.5; DB 1; Length 139;
Best Local Similarity 70.2%; Pred. No. 1.5e-27;
Matches 87; Conservative 10; Mismatches 26; Indels 1; Gaps 1;

QY 125 GGSEVVOLOQSGPELVKPGASVYKISCKDSGYAFNSMMWVWVQRPQGGLEWIGRTYPPGDSNN 184
DB 16 GVHSQVQLOQPAEVLVPGASVYKLSCKASGYFTFTSYMMHWVQRPQGGLEWIGRTIDPNSG 75
QY 185 DSNYNGKEFGKALITADKSSSTAYWQSLTSVDSAVYFCARSGLLRYA-MYWGQGTSTV 243
DB 76 GTTYNHEFRSKALITIDKSSSTAYWQSLTSBDSAVYFCARYGRY-FDYWGQGTTLT 135
QY 244 TVSS 247
DB 136 TVSS 139

RESULT 10
HV03_MOUSE STANDARD; PRT; 120 AA.

AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 1g heavy chain V region 36-65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8131846; Pubmed=6186498;
RA Stekevitz M., Geffer M.L., Brodeur P., Riblet R.,
RA Marshak-Rothstein A.;
RT "The genetic basis of antibody production: the dominant anti-arsenate
idiotypic response of the strain A mouse."
RT Eur. J. Immunol. 12:1023-1032(1982).
CC -1- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC SEGMENT, JH2.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 111 IG-LIKE.
FT NON TER 120 120
SQ SEQUENCE 120 AA; 13307 MW; FFO4BA167B854AF CRC64;

Query Match 32.7%; Score 430; DB 1; Length 120;
Best Local Similarity 71.7%; Pred. No. 8.1e-27;
Matches 86; Conservative 9; Mismatches 23; Indels 2; Gaps 1;

QY 130 VOLOOSGPELVKPGASVYKISCKDSGYAFNSMMWVWVQRPQGGLEWIGRTYPPGDSNN 189
DB 1 VOLOOSGPELVKPGASVYKLSCKASGYFTFTSYMMHWVQRPQGGLEWIGRTIDPNSG 75
QY 190 GKFGKALITADKSSSTAYWQSLTSVDSAVYFCARSGLL-RYANDYWGQGTSTVSS 247
DB 61 EKFGKTLITVDKSSSTAYWQSLTSBDSAVYFCARSGVYGGSYFDYWGQGTTLTVSS 120

RESULT 11
HV11_MOUSE STANDARD; PRT; 137 AA.

AC P01755;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 1g heavy chain V region 543 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; Pubmed=6788376;
RA Botchwell A.L.M., Paskind M., Reith W., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NpB family of
antibodies: somatic mutation evident in a gamma 2a variable region."
RT Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THE GAMMA-2A CHAIN WEA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----

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CC BMB; J00539; AAA38172.1; -.
DR PIR; A02038; GZMS43.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 137
FT DOMAIN 20 49
FT DOMAIN 50 54
FT DOMAIN 55 68
FT DOMAIN 69 85
FT DOMAIN 86 117
FT DOMAIN 118 122
FT DOMAIN 123 137
FT DISULFID 41 115
FT NON TER 137 137
SQ SEQUENCE 137 AA; 15200 MW; ADD5881BF448BEC9 CRC64;

Query Match 32.4%; Score 426.5; DB 1; Length 137;
Best Local Similarity 69.9%; Pred. No. 1.8e-26;
Matches 86; Conservative 8; Mismatches 28; Indels 1; Gaps 1;

QY 125 GGSEVVOLOQSGPELVKPGASVYKISCKDSGYAFNSMMWVWVQRPQGGLEWIGRTYPPGDSNN 184
DB 16 GVHSQVQLOQPAEVLVPGASVYKLSCKASGYFTFTSYMMHWVQRPQGGLEWIGRTIDPNSG 75
QY 185 DSNYNGKEFGKALITADKSSSTAYWQSLTSVDSAVYFCARSGLLRYA-MYWGQGTSTV 244
DB 76 GTTYNHEFRSKALITIDKSSSTAYWQSLTSBDSAVYFCARYGRY-FDYWGQGTTLT 134
QY 245 VSS 247
DB 135 VSS 137

RESULT 12
HV52_MOUSE STANDARD; PRT; 117 AA.
AC P06377;
DT 01-JAN-1988 (Rel. 06, Created)

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DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region VH558 A1/A4 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=8509340; PubMed=2578321;
RA Vancopoulos G.D., Alt F.W.;
RT "Developmentally controlled and tissue-specific expression of
RL rearranged VH gene segments.";
RL Cell 40:271-281(1985).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M13787; AAA38499.1; -.
CC PIR; A02029; HVM5A1.
CC HSSP; P01810; 2FBJ.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_V.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG_LIKE; 1.
CC Immunoglobulin V region; Signal.
CC SIGNAL 1 19
CC CHAIN 20 117 IG HEAVY CHAIN V REGION VH558 A1/A4.
CC DOMAIN 20 49 FRAMEWORK-1.
CC DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
CC DOMAIN 55 68 FRAMEWORK-2.
CC DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
CC DOMAIN 86 117 FRAMEWORK-3.
CC DISULFID 41 115 BY SIMILARITY.
CC NON TER 117 117
CC SEQUENCE 117 AA; 12971 MW; 8B0BC13885DFC9D CRC64;

Query Match 32.1%; Score 423; DB 1; Length 117;
Best Local Similarity 79.0%; Pred. No. 2.8e-26; Indels 0; Gaps 0;
Matches 83; Conservative 6; Mismatches 16;

QY 122 GGGGGGSEVQLQSGPELVKPGASVKISCKDQGYAFNMMWVKQPGQGLEWIGRIYP 181
DB 13 GTAGVHCQVQLQSGPELVKPGALVKISCKASGYTFSTYDINWKQPGQGLEWIGRIYP 72
QY 182 GDGSNNGKFEKRAILITADKSSSTAYWQLSLTSVDSAVYFCAR 226
DB 73 GDGSNNGKFEKRAILITADKSSSTAYWQLSLTSVDSAVYFCAR 117

RESULT 13
HVS_MOUSE STANDARD; PRT; 117 AA.
AC P01750;
DT 21-JUL-1986 (Rel. 01, Created)
DT 15-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 102 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6;
RA MEDLINE=81234548; PubMed=6788376;
RA Botwell A.L.M., Paekind W., Reth W., Imanishi-Kari T., Rajewsky K.,

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RA Baltimore D.;
RT "Heavy chain variable region contribution to the NpB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1 MISCELLANEOUS; THIS GERM-LINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NpB ANTIBODIES.
CC PIR; A02032; HVM502.
CC HSSP; P01810; 2FBJ.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_V.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG_LIKE; 1.
CC Immunoglobulin V region; Signal.
CC SIGNAL 1 19
CC CHAIN 20 117 IG HEAVY CHAIN V REGION 102.
CC DOMAIN 20 49 FRAMEWORK-1.
CC DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
CC DOMAIN 55 68 FRAMEWORK-2.
CC DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
CC DOMAIN 86 117 FRAMEWORK-3.
CC DISULFID 41 115 BY SIMILARITY.
CC NON TER 117 117
CC SEQUENCE 117 AA; 12867 MW; 740A65D851FCAC8 CRC64;

Query Match 32.0%; Score 421; DB 1; Length 117;
Best Local Similarity 79.2%; Pred. No. 3.9e-26; Indels 0; Gaps 0;
Matches 80; Conservative 6; Mismatches 15;

QY 125 GGGSEVQLQSGPELVKPGASVKISCKDQGYAFNMMWVKQPGQGLEWIGRIYPDG 184
DB 16 GVSHVQLQPGALVKPGASVKISCKASGYTFSTYDINWKQPGQGLEWIGRIHPDS 75
QY 185 DSNNGKFEKRAILITADKSSSTAYWQLSLTSVDSAVYFCAR 225
DB 76 DTVNQKFEKRAILITADKSSSTAYWQLSLTSVDSAVYFCAR 116

RESULT 14
HVS_MOUSE STANDARD; PRT; 138 AA.
AC P03980;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region TPC 1017 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=84248078; PubMed=6429663;
RA Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
RA Tucker F.W.;
RT "Illegitimate recombination generates a class switch from C mu to C
RT delta in an IgD-secreting plasmacytoma.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
CC PIR; A02033; HVM5T7.
CC HSSP; P01810; 2FBJ.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_V.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG_LIKE; 1.
CC Immunoglobulin V region; Signal.
CC SIGNAL 1 20
CC CHAIN 21 138 IG HEAVY CHAIN V REGION TPC 1017.
CC DOMAIN 21 49 FRAMEWORK-1.
CC DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
CC DOMAIN 55 68 FRAMEWORK-2.
CC DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
CC DOMAIN 86 117 FRAMEWORK-3.

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FT DOMAIN 118 127 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 128 138 FRAMEWORK-4.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 138 138
SQ SEQUENCE 138 AA; 15576 MW; 74815784690788E CRC64;

Query Match 31.8%; Score 419; DB 1; Length 138;
Best Local Similarity 68.3%; Pred. No. 6.7e-26;
Matches 82; Conservative 11; Mismatches 27; Indels 0; Gaps 0;

QY 128 SEVQLQDSGPGLPVGASVKISCKDGSYAFNSNMWVKORPGQGLEWIGRIYPGDSN 187
DB 19 SVQLQDSGPGLPVGASVQLSCASGHTFTNWMVKORPGQGLEWIGELINPDGRSN 78
QY 188 YNKEFGKALITADKSSSTAYMQLSLTSVDSAVYFCARSGLRVAMDYWGQSTVTVSS 247
DB 79 YNKEFGKALITADKSSSTAYMQLSLTSVDSAVYFCARSGLRVAMDYWGQSTVTVSS 138

RESULT 15

HV13_MOUSE STANDARD; FRT; 117 AA.
ID HV13_MOUSE
AC P01757;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region J558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=80078170; PubMed=6765983;
RA Schilling J., Clevinger B., Davie J.M., Hood L.;
RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
rearrangements in heavy chain V-region gene segments."
RL Nature 283:35-40(1980).
CC -1- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
CC WHICH OCCUR IN THE D AND J SEGMENTS.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A26242; MHMSJ5.
DR HSSP; P01789; MCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGY_1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Immunoglobulin V region.
KW DOMAIN 1 116 IG-LIKE.
FT DISULFID 22 96 BY SIMILARITY.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 13024 MW; 292E2AF4B8447E41 CRC64;

Query Match 31.5%; Score 415; DB 1; Length 117;
Best Local Similarity 70.0%; Pred. No. 1.1e-25;
Matches 84; Conservative 10; Mismatches 22; Indels 4; Gaps 2;

QY 129 EVQLQDSGPGLPVGASVKISCKDGSYAFNSNMWVKORPGQGLEWIGRIYPGDSN 188
DB 1 EVQLQDSGPGLPVGASVQLSCASGHTFTNWMVKORPGQGLEWIGELINPDGRSN 60
QY 189 YNKEFGKALITADKSSSTAYMQLSLTSVDSAVYFCARSGLRVAMDYWGQSTVTVSS 247
DB 61 YNKEFGKALITADKSSSTAYMQLSLTSVDSAVYFCARSGLRVAMDYWGQSTVTVSS 117

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OW protein - protein search, using sw model

Run on: April 22, 2004, 11:49:33 ; Search time 36 Seconds
(without alignment)
2164.805 Million cell updates/sec

Title: US-10-620-049-25
Perfect score: 1316
Sequence: 1 D10MTGTTSLSLASLGDRTV.....GLLRVMDYWGQGTSTVTS 247

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP_invertebrate:*
6: SP_mammal:*
7: SP_mmc:*
8: SP_organelle:*
9: SP_phase:*
10: SP_plant:*
11: SP_rodent:*
12: SP_virus:*
13: SP_vertebrate:*
14: SP_unclassified:*
15: SP_virus:*
16: SP_bacteriap:*
17: SP_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	535	40.7	614	11	Q7TMT6 mus musculu
2	524.5	39.9	234	11	Q91WF8 mus musculu
3	486	36.9	111	11	Q9D9B8 mus musculu
4	483.5	36.7	110	11	Q9JL83 mus musculu
5	478	36.3	474	11	Q8R3H6 mus musculu
6	477.5	36.3	233	11	Q91WS9 mus musculu
7	471	35.8	142	11	Q924Q1 mus musculu
8	470	35.7	481	11	Q91WT1 mus musculu
9	469.5	35.7	145	11	Q924Q6 mus musculu
10	465.5	35.4	145	11	Q924Q9 mus musculu
11	464.5	35.3	145	11	Q924R1 mus musculu
12	464.5	35.3	145	11	Q924R4 mus musculu
13	463.5	35.2	118	11	Q921C4 mus musculu
14	461	35.0	146	11	Q924Q3 mus musculu
15	459.5	34.9	234	11	Q8R062 mus musculu
16	459.5	34.9	482	11	Q8K172 mus musculu

17	458.5	34.8	145	11	Q924P7 mus musculu
18	458	34.8	473	11	Q9D8L4 mus musculu
19	456.5	34.7	143	11	Q924R0 mus musculu
20	455.5	34.6	488	11	Q8K0F2 mus musculu
21	454	34.5	140	11	Q924R2 mus musculu
22	452	34.3	146	11	Q924R8 mus musculu
23	450.5	34.2	613	11	Q8VCX7 mus musculu
24	449.5	34.2	143	11	Q924Q0 mus musculu
25	446	33.9	117	11	Q9QX69 mus musculu
26	446	33.9	480	11	Q8K0Z4 mus musculu
27	445.5	33.9	473	11	Q99125 mus musculu
28	444	33.7	168	11	Q8VDC9 mus musculu
29	440.5	33.5	143	11	Q924P9 mus musculu
30	440	33.4	140	11	Q924P8 mus musculu
31	439.5	33.4	137	11	Q924R5 mus musculu
32	439	33.4	146	11	Q924Q8 mus musculu
33	436.5	33.2	141	11	Q924Q4 mus musculu
34	436.5	33.2	463	11	Q991C4 mus musculu
35	436	33.1	142	11	Q924Q2 mus musculu
36	435.5	33.1	145	11	Q924Q7 mus musculu
37	435	33.1	144	11	Q924P5 mus musculu
38	433.5	32.9	136	11	Q7TPE3 mus musculu
39	433	32.9	470	11	Q7TMK1 mus musculu
40	432.5	32.9	110	11	Q9JL77 mus musculu
41	431.5	32.8	143	11	Q924P6 mus musculu
42	430.5	32.7	145	11	Q924R3 mus musculu
43	429.5	32.6	143	11	Q924Q5 mus musculu
44	428.5	32.6	143	11	Q924R7 mus musculu
45	428.5	32.6	243	11	Q7TQM2 mus musculu

ALIGNMENTS

RESULT 1

Q7TMT6 PRELIMINARY; PRT; 614 AA.

AC Q7TMT6;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Boraldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.O., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton B., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grumman J., Schmitt J., Myers R.M., Butterfield Y.S.,
RA Krzywicki W.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra W.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;

RA Strausberg R.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC053409; AAHS3409.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 614 AA; 67746 MW; 839BAF3B8D124F89 CRC64;

Query Match 40.7%; Score 535; DB 11; Length 614;
 Best Local Similarity 82.9%; Pred. No. 5e-37; 14; Indels 0; Gaps 0;
 Matches 102; Conservative 7; Mismatches 14; Indels 0; Gaps 0;
 QY 125 GGGSEVQLQSGPGLVFKGASVKISKDSGYAFNSMNMVVKQPGQGLEWIGRIYFGDG 184
 DB 16 GVHSQVLQSGPGLVFKGASVKISKDSGYAFNSMNMVVKQPGQGLEWIGRIYFGDG 75
 QY 185 DSNYNGKFGKAILTADKSSSTAYMQLSLTSVDSAVYFCARSGLLRYAMDYNGGTSVT 244
 DB 76 DTNYNGKFGKATLTADKSSSTAYMQLSLTSVDSAVYFCARDYSGSYFYAYWGQGTILT 135
 QY 245 VSS 247
 DB 136 VSA 138

RESULT 2
 Q91WF8 PRELIMINARY; PRT; 234 AA.
 ID Q91WF8
 AC Q91WF8
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon;
 RA Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC015292; AAH15292.1; -.
 DR GO; GO:0005622; C:intracellular; IEA.
 DR GO; GO:0005840; C:ribosome; IEA.
 DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
 DR GO; GO:0006412; F:protein biosynthesis; IEA.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR InterPro; IPR001865; Ribosomal_s2.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS00835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; 1.
 DR PROSITE; PS00962; RIBOSOMAL_S2_1; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 234 AA; 25929 MW; B0D0B0S6EB7812D2 CRC64;

Query Match 39.9%; Score 524.5; DB 11; Length 234;
 Best Local Similarity 52.0%; Pred. No. 1.2e-36;
 Matches 116; Conservative 12; Mismatches 44; Indels 51; Gaps 4;
 QY 1 DIQWTTSSLSASLGRVTVCRAQDRIYNLWYQKPDGTVKPLIYTTSLRLLPGVPS 60
 DB 21 DIQWTTSSLSASLGRVTVCRAQDRIYNLWYQKPDGTVKPLIYTTSLRLLPGVPS 80
 QY 61 RFGSGSGTDYSLTINLEQEDIGTVFCQGNTPPMTFGGTYKLEIKRGSGSGDGGSGG 120
 DB 81 RFGSGSGTDYSLTINLEQEDIGTVFCQGNTPPMTFGGTYKLEIKRGSGSGDGGSGG 128
 QY 121 GGGGGSEVQLQSGPGLVFKGASVKISKDSGYAFNSMNMVVKQPGQGLEWIGRIY 180
 DB 129 --ADAAPTIVSIFPPSPSEQLTSGASV-----VCFLNNFY 160

QY 181 PG-----DGSNYNGKFGKAILTADKSSSTAYMQLSLT 215
 DB 161 PKDINVKWKIDGSRONGVLNS---WTDQDSKDSYMSSTILT 200

RESULT 3
 Q9D9B8 PRELIMINARY; PRT; 111 AA.
 ID Q9D9B8
 AC Q9D9B8
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Adult male testis cDNA, RIKEN full-length enriched library.
 DE clone:1700110L11, full insert sequence.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RC MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinesawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Komno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Ioyo-oka K., Wang K.H., Weitz C., Whittaker C., Wiiming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kontecki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 DR EMBL; AK007163; BAB24877.1; -.
 DR HSSP; P01810; 2FBJ
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 SQ SEQUENCE 111 AA; 11976 MW; 874DDF7BD98BD7B2 CRC64;
 Query Match 36.9%; Score 486; DB 11; Length 111;
 Best Local Similarity 90.2%; Pred. No. 8.4e-34;
 Matches 92; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
 QY 125 GGGSEVQLQSGPGLVFKGASVKISKDSGYAFNSMNMVVKQPGQGLEWIGRIYFGDG 184
 DB 3 GVHSQVLQSGPGLVFKGASVKISKDSGYAFNSMNMVVKQPGQGLEWIGRIYFGDG 62
 QY 185 DSNYNGKFGKAILTADKSSSTAYMQLSLTSVDSAVYFCAR 226
 DB 63 DTNYNGKFGKATLTADKSSSTAYMQLSLTSVDSAVYFCAR 104

RESULT 4
 Q9JL83 PRELIMINARY; PRT; 110 AA.
 ID Q9JL83
 AC Q9JL83
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Anti-myosin immunoglobulin heavy chain variable region
 DE (Fragment).

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/c;
RX MEDLINE=20448942; PubMed=1092488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.,
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin.";
RL Infect. Immun. 68:5803-5808 (2000).
DR EMBL; AF206023; AAF69321.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 110
SQ SEQUENCE 110 AA; 12052 MW; 8486F2AD219AF95E CRC64;
Query Match 36.7%; Score 483.5; DB 11; Length 110;
Best Local Similarity 83.9%; Pred. No. 1.4e-33;
Matches 94; Conservative 7; Mismatches 8; Indels 3; Gaps 2;
QY 137 PELVPGASVKISCKDSGYAFNSWNWVKQPGGLEWIGRIYFGDSNYNGKFEKGA 196
Db 1 PELVPGASVKISCKASGYTFNSWNWVKLRPGQGLEWIGRIYFGDGDYNGKFEKGA 60
QY 197 ILTADSSSTAYNQLSSLTSDVSAVFCARSGL-LRYANDYNGQGTSTVTS 247
Db 61 TLTADSSSTAYNQLSSLTSDVSAVFCARSNDVRFPA--YWGQTLTVTVA 110
RESULT 5
Q8R3H6 PRELIMINARY; PRT; 474 AA.
AC Q8R3H6;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN AU044919.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025447; AAH25447.1; -.
DR MGD; MGI:2144967; AU044919.
DR GO; GO:0005489; P-electron transporter activity; IEA.
DR GO; GO:0006118; P-electron transport; IEA.
DR InterPro; IPR003345; Cytochrome_B5.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00190; CYTOCHROME C; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 474 AA; 51748 MW; 8608B57C6CD2874A CRC64;
Query Match 36.3%; Score 478; DB 11; Length 474;
Best Local Similarity 74.0%; Pred. No. 2.5e-32;
Matches 91; Conservative 14; Mismatches 18; Indels 0; Gaps 0;

QY 125 GGSSEVOIQSGPELVKPGASVKISCKDSGYAFNSWNWVKQPGGLEWIGRIYFGDG 184
Db 16 GVHSQVQLQSGPELVKPGASVKISCRASGYAFNSWNWVKRPRGKLEWIGRIYFGDG 75
QY 185 DSNYNGKFEKAILTADSSSTAYNQLSSLTSDVSAVFCARSGLLRANDYNGQGTSTV 244
Db 76 DTHYSGKFGKAKLTADSSVTAFQLTSLTSDSAVFCARDSDYDGYFDDMQGATVT 135
QY 245 VSS 247
Db 136 VSS 138
RESULT 6
Q91WS9 PRELIMINARY; PRT; 233 AA.
AC Q91WS9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013496; AAH13496.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 233 AA; 25781 MW; B1C184DA149A16EB CRC64;
Query Match 36.3%; Score 477.5; DB 11; Length 233;
Best Local Similarity 48.9%; Pred. No. 1.1e-32;
Matches 109; Conservative 11; Mismatches 52; Indels 51; Gaps 4;
QY 1 DIQMTQTSSLSASLGDRTVTSRASQDIRNYLNWYQKPDGTVKFLIYYTSRLPGVPS 60
Db 20 DIQMTQTSSLSASLGDRTVTSRASQDIRNYLNWYQKPDGTVKFLIYYTSRLPGVPS 79
QY 61 RFGSGSGTDYSLTINLEQRIQYFCQGNTPPWTFGGGTKEIKRKGSGSGSGSGG 120
Db 80 RFGSGSGTDYSLTINLEPEDIATYCCQRYLFWTFGGGTKEIKR----- 127
QY 121 GSGSGSGSVQLQSGPELVKPGASVKISCKDSGYAFNSWNWVKQPGGLEWIGRIY 180
Db 128 --ADAAPTIVSIFPPSSEQLTSGASV-----VCFLLNFF 159
QY 181 PG-----DGSNYNGKFEKAILTADSSSTAYNQLSSLT 215
Db 160 PKDINVKWKIDGSRQNGVLNS---WTDQDSKDSYMSSTLT 199
RESULT 7
Q924Q1 PRELIMINARY; PRT; 142 AA.
AC Q924Q1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE V23-D-J-C mu protein (Fragment).
GN V23-D-J-C MU.

OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	NCBI_TaxID=10090;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=C57BL/6;	
RA	Kozono Y., Kozono H., Azuma T.,	
RT	"Direct Estimation of Relative Affinity by Flow Cytometry Reveals	
RT	Affinity Maturation of B Cell Antigen Receptors in Response to (4-	
RT	Hydroxy-3-Nitrophenyl)Acetyl (NP)."	
RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; AB069913; BAB63292.1; -.	
DR	PIR; F33932; F33932.	
DR	PIR; I28833; I28833.	
DR	PIR; PH1156; PH1156.	
DR	PIR; PH1158; PH1158.	
DR	InterPro; IPR007110; IG-like.	
DR	InterPro; IPR003596; IG_v.	
DR	Pfam; PF00047; Ig; 1.	
DR	SMART; SM00406; IGV; 1.	
DR	PROSITE; PS00406; IGV; 1.	
DR	PROSITE; PS50835; IG LIKE; 1.	
FT	NON_TER 1	
FT	NON_TER 142	
FT	NON_TER 142	
SQ	SEQUENCE 142 AA; 15622 MW; 24A265CE4EA4318B CRC64;	
Query Match 35.7%; Score 471; DB 11; Length 142;		
Best Local Similarity 77.3%; Pred. No. 2.2e-32;		
Matches 92; Conservative 7; Mismatches 18; Indels 2; Gaps 1;		
QY	129 EVQLQSGPELVKPGASVKISCKDGYAFNSWMNWVKRPGQGLEWIGRIYPGGDSNY 188	
DB	1 QVQLQPGELVKPGASVKLSCKASGYTFTSYMHVWVKRPGQGLEWIGNINPNSGGTNY 60	
QY	189 NGKFEKAILTADKSSSTAYMQLSSLTSVDSAVYFCARSGLLRYAMDYWGQTSVTVS 247	
DB	61 NERFKSKATLTVDKSSSTAYMQLSSLTSVDSAVYFCAREGW--EAMDYWGQTSVTVS 117	
RESULT 8		
Q91WT1	PRELIMINARY; PRT; 481 AA.	
ID	Q91WT1	
AC	Q91WT1;	
DT	01-DEC-2001 (TrEMBLrel. 19, Created)	
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)	
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)	
DE	Hypothetical protein.	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	NCBI_TaxID=10090;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	Tissue=Colon;	
RA	Straussberg R.;	
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; BC013490; AAH13490.1; -.	
DR	InterPro; IPR007110; IG-like.	
DR	InterPro; IPR003006; IG_MHC.	
DR	InterPro; IPR003596; IG_v.	
DR	Pfam; PF00047; Ig; 4.	
DR	SMART; SM00406; IGV; 1.	
DR	PROSITE; PS50835; IG LIKE; 4.	
DR	PROSITE; PS0290; IG_MHC; 2.	
KW	Hypothetical protein.	
SQ	SEQUENCE 481 AA; 52105 MW; 97DF68D159463F65 CRC64;	
Query Match 35.7%; Score 470; DB 11; Length 481;		
Best Local Similarity 73.0%; Pred. No. 1.2e-31;		
Matches 92; Conservative 11; Mismatches 21; Indels 2; Gaps 1;		
QY	122 GSGGGSEVQLQSGPELVKPGASVKISCKDGYAFNSWMNWVKRPGQGLEWIGRIY 191	

DB	13 GTAGVQCQVQLQSGPELVKPGASVKISCKASGYTFTSYIHWVKRPGQGLVWIGMIYP 72	
QY	182 GGDGSDNYKFGKAILTADKSSSTAYMQLSSLTSVDSAVYFCARSGLLRYAMDYWGQGT 241	
DB	73 GGDGNTKYNKFKGKTLTADKSSSTAYMQLSSLTSVDSAVYFCARSG--GWAFDYWGQGT 130	
QY	242 SVTVSS 247	
DB	131 TLTVSS 136	
RESULT 9		
Q924Q6	PRELIMINARY; PRT; 145 AA.	
ID	Q924Q6	
AC	Q924Q6;	
DT	01-DEC-2001 (TrEMBLrel. 19, Created)	
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)	
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)	
DE	VH186.2-D-J-C mu protein (Fragment).	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	NCBI_TaxID=10090;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=C57BL/6;	
RA	Kozono Y., Kozono H., Azuma T.,	
RT	"Direct Estimation of Relative Affinity by Flow Cytometry Reveals	
RT	Affinity Maturation of B Cell Antigen Receptors in Response to (4-	
RT	Hydroxy-3-Nitrophenyl)Acetyl (NP)."	
RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; AB067794; BAB63279.1; -.	
DR	PIR; F28833; F28833.	
DR	PIR; F33932; F33932.	
DR	PIR; PH1105; PH1105.	
DR	PIR; PH1108; PH1108.	
DR	PIR; PH1114; PH1114.	
DR	PIR; PH1118; PH1118.	
DR	PIR; PH1119; PH1119.	
DR	PIR; PH1125; PH1125.	
DR	PIR; PH1126; PH1126.	
DR	PIR; PH1128; PH1128.	
DR	PIR; PH1129; PH1129.	
DR	PIR; PH1131; PH1131.	
DR	PIR; PH1134; PH1134.	
DR	PIR; PH1137; PH1137.	
DR	PIR; PH1139; PH1139.	
DR	PIR; PH1142; PH1142.	
DR	PIR; PH1144; PH1144.	
DR	PIR; PH1147; PH1147.	
DR	PIR; PH1149; PH1149.	
DR	PIR; PH1150; PH1150.	
DR	PIR; PH1151; PH1151.	
DR	PIR; PH1152; PH1152.	
DR	PIR; PH1153; PH1153.	
DR	InterPro; IPR007110; IG-like.	
DR	InterPro; IPR003596; IG_v.	
DR	Pfam; PF00047; Ig; 1.	
DR	SMART; SM00406; IGV; 1.	
DR	PROSITE; PS50835; IG LIKE; 1.	
FT	NON_TER 1	
FT	NON_TER 145	
FT	NON_TER 145	
SQ	SEQUENCE 145 AA; 16011 MW; 9BC0846D40DF97EA CRC64;	
Query Match 35.7%; Score 469.5; DB 11; Length 145;		
Best Local Similarity 76.7%; Pred. No. 3e-32;		
Matches 92; Conservative 7; Mismatches 20; Indels 1; Gaps 1;		
QY	129 EVQLQSGPELVKPGASVKISCKDGYAFNSWMNWVKRPGQGLEWIGRIYPGGDSNY 188	
DB	1 QVQLQPGELVKPGASVKLSCKASGYTFTSYMHVWVKRPGQGLEWIGRIDPNSSGGTKY 60	
QY	189 NGKFEKAILTADKSSSTAYMQLSSLTSVDSAVYFCARSGLLR-YAMDYWGQTSVTVS 247	

[illegible]


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DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 146
SQ SEQUENCE 146 AA; 16136 MW; CEA8DD6E1955807F CRC64;

Query Match      35.0%; Score 461; DB 11; Length 146;
Best Local Similarity 75.2%; Pred. No. 1.6e-31;
Matches 91; Conservative 7; Mismatches 21; Indels 2; Gaps 1;

QY 129 EVQLQQSGPELVKPGASVKISCKDGYAFNFSNMNWKQRPQGQGLEWIGRIYFGDSDSNY 188
Db 1 QVQLQQPGAEVLKPGASVKLSKASGYTFTSYWVHWKQRPGRGLEWIGRIDPNSGGTKY 60
QY 189 NGKFEKGKAILTADKSSSTAYNQLSLSVDSAVTFCARSS--GLLRVANDYWGQTSVTVS 246
Db 61 NEKFKSKATLVDPSPSTAYNQLSLSVDSAVTYCARSLSDYGYDYANDYWGQTSVTVS 120
QY 247 S 247
Db 121 S 121

RESULT 15
QSR062 PRELIMINARY; PRT; 234 AA.
AC QSR062;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC027418, RAH27418.1; -.
DR InterPro; IPR007110; IG_LIKE.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25857 MW; 4EB08C81426AEAB1 CRC64;

Query Match      34.9%; Score 459.5; DB 11; Length 234;
Best Local Similarity 48.0%; Pred. No. 3.8e-31;
Matches 107; Conservative 13; Mismatches 52; Indels 51; Gaps 4;

QY 1 DIQMTQTSSLSASLGDRVTVSCRASODIRNVLNWKQKPGDGVKELIYTSRLPGVPS 60
Db 21 DIQMTQTSSLSASLGDRVTVSCRASQGISNVLNWKQKPGDGVKLLIYTSRLHSGVPS 80
QY 61 RFSGSGSDYSLTINNLEQEDIGTYFCQQGNTPPTFGCGTKLEIKRGGSGSDGGSGG 120
Db 81 RFSGSGSGTHYSLTINNLEPEDIATYCCQYQFPPTFGSGTKLEIKR----- 128
QY 121 GSGSGGGSEVQLQQSGPELVKPGASVKISCKDGYAFNFSNMNWKQRPQGQGLEWIGRIY 180
Db 129 --ADAAPTYSIFPPSSEQLTSGGASV-----VCFLNPFY 160
QY 181 PG-----DGSNTYNGKPEKAILTADKSSSTAYNQLSSLT 215
Db 161 PKDINVKNKIDGERQRGVLS---WTDQSKDSTYSMSSTLT 200

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 22, 2004, 11:51:48 ; Search time 14 Seconds
(without alignments)
1697.093 Million cell updates/sec

Title: US-10-620-049-25

Perfect score: 1316

Sequence: 1 DIQMTQTSSLSASLGDRVT.....GILRYMDYWGQSTVTSS 247

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78:**

1: Pir1:**

2: Pir2:**

3: Pir3:**

4: Pir4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	635.5	48.3	287	PC4402	peB leader/Ig hea
2	542.5	41.2	119	A24672	Ig heavy chain pre
3	527.5	40.1	117	PL0237	Ig heavy chain V r
4	526	40.0	108	S69300	Ig kappa chain (cl
5	526	40.0	118	PL0231	Ig heavy chain V r
6	524.5	39.9	117	PL0235	Ig heavy chain V r
7	523	39.7	109	PH0888	Ig kappa chain V r
8	522	39.7	122	A29380	Ig kappa chain pre
9	517	39.3	108	S69303	Ig kappa chain (cl
10	517	39.3	115	JL0080	Ig kappa chain pre
11	516.5	39.2	108	S38862	Ig kappa chain V r
12	515.5	39.2	117	PL0234	Ig heavy chain V r
13	515	39.1	126	A34904	Ig kappa chain pre
14	513	39.0	108	B26405	Ig kappa chain V r
15	509.5	38.7	115	PL0238	Ig heavy chain V r
16	508.5	38.6	107	S69301	Ig kappa chain (cl
17	508	38.6	108	KVMSAR	Ig kappa chain V r
18	507	38.6	108	C26405	Ig kappa chain V r
19	507	38.5	128	A26406	Ig kappa chain V r
20	505	38.4	108	S19370	Ig kappa chain V r
21	505	38.4	108	S69302	Ig kappa chain (cl
22	502	38.1	107	B28044	Ig kappa chain V r
23	502	38.1	107	A28044	Ig kappa chain V r
24	500	38.0	108	PL0282	Ig kappa chain V r
25	500	38.0	127	PH1224	Ig kappa chain pre
26	495.5	37.7	107	S69306	Ig kappa chain (cl
27	488	37.1	112	PL0232	Ig heavy chain V r
28	486	36.9	138	E32513	Ig heavy chain pre
29	485	36.9	107	S32188	Ig kappa chain V r

ALIGNMENTS

RESULT 1

PC4402

peB leader/Ig heavy chain anti-NP/linker type 205/alkaline phosphatase fusion protein

C;Species: synthetic

C;Date: 06-Nov-1998 #sequence_revision 06-Nov-1998 #text_change 06-Nov-1998

C;Accession: PC4402

R;Suzuki, C.; Ueda, H.; Suzuki, E.; Nagamune, T.

J. Biochem. 122, 322-329, 1997

A;Title: Construction, bacterial expression, and characterization of hapten-specific si

A;Reference number: PC4402

A;Accession: PC4402

A;Molecule type: DNA

A;Residues: 1-287 <SUZ>

C;Keywords: fusion protein

Query Match 48.3%; Score 635.5; DB 4; Length 287;
Best Local Similarity 53.3%; Pred. No. 3e-36;
Matches 138; Conservative 24; Mismatches 82; Indels 15; Gaps 5;

Qy 1 DIQMTQT-TSSLSASLGDRVTVSCRSQ---DIRNLNWKQKPDGTVKFLIYVTSRLLP 56
Db 24 DIQAVVTOESALTTPGETVLTCTCSSTGAVTTSYANWVQEKPDHLPFTGLIGGTNNRAP 83
Qy 57 GVPSPFSGSGSGTDSLTLNNLEQEDIGTYFCQCGNTPTPTFGGCTKLEI-----KRG 109
Db 84 GVPARESGSLIGDKAALITGTAQTEDEALFYCALWYNHNVFVGCTKLTVLSSADDAKDD 143
Qy 110 GGGSDGGSGGGSGGGSEVLOQSGPELVKPGASVKISCKDSGYAFNSSWNVKQRP 169
Db 144 DAKDDAKKDDAKDDG---QVQLQPGAEVLKPGASVKLSCKASGYTFTSYMHWKQRP 200
Qy 170 GQGLEWIGRIYPGDGDSDNYNKFEGKAILTADKSSSTAYMQLSSLTSDSAVYFCARSGL 229
Db 201 GRGLEWIGRIDNSGGTKYNEKFKSKATLTVDKPSSTAYMQLSSLTSDSAVYCYRDY 260
Qy 230 LRYA-MDYWGQSTVTSS 247
Db 261 YGSSYFDYWGQSTTLTVSS 279

RESULT 2

A24672

Ig heavy chain precursor V region (VMU-3.2) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 23-Jul-1999

C;Accession: A24672

R;Winter, E.; Radbruch, A.; Krawinkel, U.

EMBO J. 4, 2861-2867, 1985

A;Reference number: A91022; PMID:86055722; PMID:2998759

A;Accession: A24672

A;Molecule type: DNA

A;Residues: 1-119 <WIN>

A;Cross-references: GB:X03088; NID:G52378; PIDN:CAA36881.1; PID:G773578
A;Note: this sequence was determined from the germline gene
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; chain V region
F;4-119/Product: Ig heavy chain V region VNU-3.2 #status predicted <MAT>
F;18-101/Domain: immunoglobulin homology <IMM>

Query Match 41.2%; Score 542.5; DB 2; Length 119;
Best Local Similarity 85.5%; Pred. No. 2.6e-30;
Matches 103; Conservative 7; Mismatches 7; Indels 3; Gaps 1;

QY 128 SEVQLQSGPELVKPGASVKISCKDQSGYAFNSWNNWVKQRPQGQLEWIGRIYPGDGSN 187
DB 3 SQVQLQSGPELVKPGASVKISCKASGYAFSSWNNWVKQRPQGQLEWIGRIYPGDGSN 62
QY 188 YNGKFEKATLTADKSSSTAYNQLSLTSVDSAVYFCARSGLRLRYAMDYWGQGTSTVYS 247
DB 63 YNGKFKGKATLTADKSSSTAYNQLSLTSVDSAVYFCARD---YWGSDYWGQGTSTVYS 119

RESULT 3
PL0237
Ig heavy chain V region (anti-DNA, 1A11VH) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
C;Accession: PL0237
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A;Reference number: PL0231; MUID:90111618; PMID:2104919
A;Accession: PL0237
A;Molecule type: mRNA
A;Residues: 1-117 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-30/Region: framework 1
F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
F;36-49/Region: complementarity-determining 2
F;50-66/Region: complementarity-determining 3
F;67-98/Region: framework 3
F;99-109/Region: complementarity-determining 3
F;110-117/Region: framework 4

Query Match 40.1%; Score 527.5; DB 2; Length 117;
Best Local Similarity 85.5%; Pred. No. 2.6e-29;
Matches 100; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

QY 129 EVQLQSGPELVKPGASVKISCKDQSGYAFNSWNNWVKQRPQGQLEWIGRIYPGDGSNY 188
DB 1 QVQLQSGPELVKPGGSKISCKASGYAFSSWNNWVKQRPQGQLEWIGRIYPGDGSNY 60
QY 189 NGKFEKATLTADKSSSTAYNQLSLTSVDSAVYFCARS-GLRLRYAMDYWGQGTSTV 244
DB 61 NGKFKGKATLTADKSSSTAYNQLSLTSVDSAVYFCARSKYSYVMDYWGQGTSTV 117

RESULT 4
S69900
Ig kappa chain (clone KL2.18 / KL4B10 / KL4C11) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C;Accession: S69900; S69907; S69908
R;Wysocki, L.J.; Creadon, G.; Lehmann, K.R.; Cambier, J.C.
Immunology 75, 116-121, 1992
A;Title: B-cell proliferation initiated by Ia cross-linking and sustained by interleukin
A;Reference number: S69900; MUID:92165291; PMID:1537587
A;Accession: S69900
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-108 <WYS>
A;Cross-references: EMBL:X55041; NID:G511023; PIDN:CAA38881.1; PID:G511024
A;Accession: S69907

A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-108 <WY2>
A;Cross-references: EMBL:X55048; NID:G511037; PIDN:CAA38888.1; PID:G511038
A;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; chain V region
F;4-119/Product: Ig heavy chain V region VNU-3.2 #status predicted <MAT>
F;18-101/Domain: immunoglobulin homology <IMM>

Query Match 40.0%; Score 526; DB 2; Length 108;
Best Local Similarity 92.8%; Pred. No. 3e-29;
Matches 100; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQWTTTSLASLSDRVTVSCRASQDIRNYLNWQQKPDGTVKLIYTSLLPGVPS 60
DB 1 DIQWTTTSLASLSDRVTVSCRASQDIRNYLNWQQKPDGTVKLIYTSLLPGVPS 60
QY 61 RFGSGSGTDYSLTINLEQEDIGTVFCQGNTPPWTFGGGTGLEIKR 108
DB 61 RFGSGSGTDYSLTINLEQEDIGTVFCQGNTPPWTFGGGTGLEIKR 108

RESULT 5
PL0231
Ig heavy chain V region (anti-DNA, D20VH) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
C;Accession: PL0231
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A;Reference number: PL0231; MUID:90111618; PMID:2104919
A;Accession: PL0231
A;Molecule type: mRNA
A;Residues: 1-118 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-30/Region: framework 1
F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
F;36-49/Region: complementarity-determining 2
F;50-66/Region: complementarity-determining 2
F;67-98/Region: framework 3
F;99-110/Region: complementarity-determining 3
F;111-118/Region: framework 4

Query Match 40.0%; Score 526; DB 2; Length 118;
Best Local Similarity 84.7%; Pred. No. 3.3e-29;
Matches 100; Conservative 7; Mismatches 9; Indels 2; Gaps 1;

QY 129 EVQLQSGPELVKPGASVKISCKDQSGYAFNSWNNWVKQRPQGQLEWIGRIYPGDGSNY 188
DB 1 QVQLQSGPELVKPGGSKISCKASGYAFSSWNNWVKQRPQGQLEWIGRIYPGDGSNY 60
QY 189 NGKFEKATLTADKSSSTAYNQLSLTSVDSAVYFCARSGLRLRYAMD--YWGQGTSTV 244
DB 61 NGKFKGKATLTADKSSSTAYNQLSLTSVDSAVYFCARSGLRLRYAMDYWGQGTSTV 118

RESULT 6
PL0235
Ig heavy chain V region (anti-DNA, 2F2VH and 4H8VH) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
C;Accession: PL0235
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A;Reference number: PL0231; MUID:90111618; PMID:2104919
A;Accession: PL0235

A:Molecule type: mRNA
A:Residues: 1-117 <SHL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-30/Region: framework 1
F:15-98/Domain: immunoglobulin homology <IMM>
F:31-35/Region: complementarity-determining 1
F:36-49/Region: framework 2
F:50-65/Region: complementarity-determining 2
F:67-98/Region: framework 3
F:99-109/Region: complementarity-determining 3
F:110-117/Region: framework 4

Query Match 39.9%; Score 524.5; DB 2; Length 117;
Best Local Similarity 84.6%; Pred. No. 4.2e-29;
Matches 99; Conservative 7; Mismatches 10; Indels 1; Gaps 1;

QY 129 EVLOQSGPGLYKPGASVKISCKDGYAFNSWVWVQKPGGLEWIGRIYPGGDSNY 188
DB 1 QVLOQSGPGLYKPGASVKISCKDGYAFNSWVWVQKPGGLEWIGRIYPGGDSNY 60

QY 189 NGKFEKALITADKSSSTAYMQLSSITSDSAVYFCARARSKYSVLDYWGQGSVT 244
DB 61 NGKFEKALITADKSSSTAYMQLSSITSDSAVYFCARARSKYSVLDYWGQGSVT 117

RESULT 7

PH0888
Ig kappa chain V region (anti-CD3) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 21-Jan-2000
C:Accession: PH0888
R:Shalaby, M.R.; Shepard, H.M.; Presta, L.; Rodriguez, M.L.; Beverley, P.C.L.; Feldmann, J. Exp. Med. 175, 217-225, 1992
A:Title: Development of humanized bispecific antibodies reactive with cytotoxic lymphocytes
A:Reference number: PH0885; MUID:92113462; PMID:1346155
A:Accession: PH0888
A:Molecule type: mRNA
A:Residues: 1-109 <SHA>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:15-90/Domain: immunoglobulin homology <IMM>

Query Match 39.7%; Score 523; DB 2; Length 109;
Best Local Similarity 91.7%; Pred. No. 4.9e-29;
Matches 99; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQTSSLSASLGDRVTVCASQDIRNLYNWYQKPDGTGKFLIYTSRLPGVPS 60
DB 1 DIQMTQTSSLSASLGDRVTVCASQDIRNLYNWYQKPDGTGKFLIYTSRLPGVPS 60

QY 61 RFGSGSGTDYSLTINLEQEDIGTYFCQGNTPPWTFGGGKLEIKR 108
DB 61 RFGSGSGTDYSLTINLEQEDIGTYFCQGNTPPWTFGGGKLEIKR 108

RESULT 8

A29380
Ig kappa chain precursor V region (AC-1001) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 21-Jan-2000
C:Accession: A29380
R:Chen, H.T.; Kabat, E.A.; Lundblad, A.; Ratcliffe, R.M. J. Biol. Chem. 262, 13579-13583, 1987
A:Title: Nucleotide and translated amino acid sequences of cDNA coding for the variable A:Reference number: A92612; MUID:98007582; PMID:3115981
A:Accession: A29380
A:Molecule type: mRNA
A:Residues: 1-122 <CHE>
A:Cross-references: GB:M17160; GB:J02815; NID:g196895; PIDN:AAA38824.1; PID:g196896
A:Note: the authors translated the codon TTC for residue 1 as Leu
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

F:30-104/Domain: immunoglobulin homology <IMM>

Query Match 39.7%; Score 522; DB 2; Length 122;
Best Local Similarity 91.7%; Pred. No. 6.4e-29;
Matches 99; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQTSSLSASLGDRVTVCASQDIRNLYNWYQKPDGTGKFLIYTSRLPGVPS 60
DB 15 DIQMTQTSSLSASLGDRVTVCASQDIRNLYNWYQKPDGTGKFLIYTSRLPGVPS 74

QY 61 RFGSGSGTDYSLTINLEQEDIGTYFCQGNTPPWTFGGGKLEIKR 108
DB 75 RFGSGSGTDYSLTINLEQEDIGTYFCQGNTPPWTFGGGKLEIKR 122

RESULT 9

S69903
Ig kappa chain (clone KL2.29 / KL2.33 / KL3.8) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C:Accession: S69903; S69904; S69905
R:Nysocki, L.J.; Creadon, G.; Lehmann, K.R.; Cambier, J.C. Immunology 75, 116-121, 1992
A:Title: B-cell proliferation initiated by Ia cross-linking and sustained by interleukin A:Reference number: S69900; MUID:92165291; PMID:1537587
A:Accession: S69903
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-108 <WYS>
A:Cross-references: EMBL:X55044; NID:g511029; PIDN:CAA38884.1; PID:g511030
A:Accession: S69904
A:Molecule type: DNA
A:Residues: 1-108 <WY2>
A:Cross-references: EMBL:X55045; NID:g511031; PIDN:CAA38885.1; PID:g511032
A:Accession: S69905
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-108 <WY3>
A:Cross-references: EMBL:X55046; NID:g511033; PIDN:CAA38886.1; PID:g511034
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:15-90/Domain: immunoglobulin homology <IMM>

Query Match 39.3%; Score 517; DB 2; Length 108;
Best Local Similarity 91.7%; Pred. No. 1.2e-28;
Matches 99; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQTSSLSASLGDRVTVCASQDIRNLYNWYQKPDGTGKFLIYTSRLPGVPS 60
DB 1 DIQMTQTSSLSASLGDRVTVCASQDIRNLYNWYQKPDGTGKFLIYTSRLPGVPS 60

QY 61 RFGSGSGTDYSLTINLEQEDIGTYFCQGNTPPWTFGGGKLEIKR 108
DB 61 RFGSGSGTDYSLTINLEQEDIGTYFCQGNTPPWTFGGGKLEIKR 108

RESULT 10

JL0080
Ig kappa chain precursor V region (anti-phenylloxazolone, 18C10) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 21-Jan-2000
C:Accession: JL0080
R:Kaartinen, M.; Rocca-Setra, J.; Maekela, O. Mol. Immunol. 25, 859-865, 1988
A:Title: Combinatorial association of V genes: one VH gene codes for three non-cross-re A:Reference number: JL0076; MUID:89096973; PMID:3211160
A:Accession: JL0080
A:Molecule type: mRNA
A:Residues: 1-115 <XAA>
A:Cross-references: GB:M27793; NID:g197161; PIDN:AAA38937.1; PID:g197162
A:Note: the authors translated the codon AGG for residue 30 as Ser
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin

F:1-6/Domain: signal sequence (fragment) #status predicted <SIG>
F:7-115/Product: Ig light chain #status predicted <NAT>
F:22-96/Domain: immunoglobulin homology <IMM>
F:30-40/Region: complementarity-determining 1
F:56-62/Region: complementarity-determining 2

Query Match 39.3%; Score 517; DB 2; Length 115;
Best Local Similarity 91.7%; Pred. No. 1.3e-28;
Matches 99; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQTSSLSASLGDRVTVCSCASQDIRNYLNWYQKPDGVTKFLIYTSRLLPVPS 60
DB 7 DIQMTQTSSLSASLGDRVTVCSCASQDIRNYLNWYQKPDGVTKFLIYTSRLHSGVPS 66
QY 61 RFGSGSGTDYSLTINNLEQEDIGTYFCQGNTPPWTFGGGKLEIKR 108
DB 67 RFGSGSGTDYSLTINNLEQEDIGTYFCQGNTPPWTFGGGKLEIKR 114

RESULT 11

Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C:Accession: S38862
R:Fischer, R.; Voss, A.; Hunziker, W.; Stierhof, Y.D.; Kreuzaler, F.
submitted to the EMBL Data Library, August 1993
A:Description: Production and cloning of TWV-specific monoclonal antibodies.
A:Reference number: S37200
A:Accession: S38862
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-108 <PIS>
A:Cross-references: EMBL:X75854; NID:g429109; PID:g429110
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Superfamily: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 39.2%; Score 516.5; DB 2; Length 108;
Best Local Similarity 90.7%; Pred. No. 1.3e-28;
Matches 98; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

QY 1 DIQMTQTSSLSASLGDRVTVCSCASQDIRNYLNWYQKPDGVTKFLIYTSRLLPVPS 60
DB 1 DVQMTQTSSLSASLGDRVTVCSCASQDIRNYLNWYQKPDGVTKFLIYTSRLHSGVPS 60
QY 61 RFGSGSGTDYSLTINNLEQEDIGTYFCQGNTPPWTFGGGKLEIK 107
DB 61 RFGSGSGTDYSLTINNLEQEDIGTYFCQGNTPPWTFGGGKLEIK 108

RESULT 12

Ig heavy chain V region (anti-DNA, 3H9VH) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
C:Accession: PLO234
R:Shlomchik, M.; Mascello, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A:Reference number: PLO231; MUID:90111618; PMID:2104919
A:Accession: PLO234
A:Molecule type: mRNA
A:Residues: 1-117 <SHL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

F:1-30/Region: framework 1
F:15-98/Domain: immunoglobulin homology <IMM>
F:31-35/Region: complementarity-determining 1
F:36-49/Region: framework 2
F:50-66/Region: complementarity-determining 2
F:67-98/Region: framework 3
F:99-109/Region: complementarity-determining 3

F:110-117/Region: framework 4

Query Match 39.2%; Score 515.5; DB 2; Length 117;
Best Local Similarity 84.6%; Pred. No. 1.7e-28;
Matches 99; Conservative 5; Mismatches 12; Indels 1; Gaps 1;

QY 129 EVQLQSGPELVKPGASVKISCKSGYAFNNSMMWVQKPGQGLEWIGRIYPGGDSNY 188
DB 1 QVQLQSGPELVKPGGSKVKISCKVGVAFSSMMWVQKPGQGLEWIGRIYPRGDINY 60
QY 189 NGKFEKAILTADKSSSTAYMQLSITSDSAVYFCARS-GELRYAMDYWGQGTSTV 244
DB 61 NGKFEKAILTADKSSSTAYMQLSITSDSAVYFCARSKYSYVNDYWGQGTSTV 117

RESULT 13

Ig kappa chain precursor V region (5-27) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 21-Jan-2000
C:Accession: A34904
R:Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
J. Biol. Chem. 265, 133-138, 1990
A:Title: Active site structure and antigen binding properties of idiotypically cross-reacting
A:Reference number: A34903; MUID:90094387; PMID:2104617
A:Accession: A34904
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-126 <BED>

C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:35-109/Domain: immunoglobulin homology <IMM>

Query Match 39.1%; Score 515; DB 2; Length 126;
Best Local Similarity 92.5%; Pred. No. 2e-28;
Matches 98; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQTSSLSASLGDRVTVCSCASQDIRNYLNWYQKPDGVTKFLIYTSRLLPVPS 60
DB 20 DIQMTQTSSLSASLGDRVTVCSCASQDIRNYLNWYQKPDGVTKFLIYTSRLHSGVPS 79
QY 61 RFGSGSGTDYSLTINNLEQEDIGTYFCQGNTPPWTFGGGKLEI 106
DB 80 RFGSGSGTDYSLTINNLEQEDIGTYFCQGNTPPWTFGGGKLEI 125

RESULT 14

Ig kappa chain V region (1F6) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 21-Jan-2000
C:Accession: B26405
R:Smith, J.A.; Margolies, M.N.
Biochemistry 26, 604-612, 1987
A:Title: Complete amino acid sequences of the heavy and light chain variable regions from

A:Reference number: A90518; MUID:87157677; PMID:3103682
A:Accession: B26405
A:Molecule type: protein
A:Residues: 1-108 <SMI>
A:Experimental source: strain A/J
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 39.0%; Score 513; DB 2; Length 108;
Best Local Similarity 91.7%; Pred. No. 2.3e-28;
Matches 99; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIQMTQTSSLSASLGDRVTVCSCASQDIRNYLNWYQKPDGVTKFLIYTSRLLPVPS 60
DB 1 DIQMTQTSSLSASLGDRVTVCSCASQDIRNYLNWYQKPDGVTKFLIYTSRLHSGVPS 60

QY 61 RFGSGSGTDYSLTINNLEQEDIGTVPCQOGNTPPWTFGGGTKLEIKR 108
|||||
Db 61 RFGSGSGTDYSLTINNLEQEDIGTVPCQOGNTPPWTFGGGTKLEIKR 108
|||||

RESULT 15
PL0238
Ig heavy chain V region (anti-DNA, 6NVH and 6QVH) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
C:Accession: PL0238
R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A
J. Exp. Med. 171, 263-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A:Reference number: PL0231; MUID:90111618; PMID:2104919
A:Accession: PL0238
A:Molecule type: mRNA
A:Residues: 1-115 <SHL>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
F:1-30/Region: framework 1
F:15-98/Domain: immunoglobulin homology <IMM>
F:31-35/Region: complementarity-determining 1
F:36-49/Region: framework 2
F:50-66/Region: complementarity-determining 2
F:67-98/Region: framework 3
F:99-107/Region: complementarity-determining 3
F:108-115/Region: framework 4

Query Match 38.7%; Score 509.5; DB 2; Length 115;
Best Local Similarity 84.5%; Pred. NO. 4.3e-28;
Matches 98; Conservative 5; Mismatches 12; Indels 1; Gaps 1;

QY 129 EYLOQSGPELYKPGASVKISKDSGYAFNSWMWVKQRPQGLEWIGRIYPGDSNY 188
:|||||
Db 1 QVLOQSGPELYKPGGSVKISKASGYAFSSWMWVKQRPQGLEWIGWYPGDGTNY 60
|||||
QY 189 NGKFEKALITADKSSSTAYMQLSLSVDSAVYFCARSGLLRYANDYWGQTSVT 244
|||||
Db 61 NGKFRGKALITADKSSSTAYMQLSLSVDSAVYFCARYRL-LPFDYWGQTTVT 115
|||||

Search completed: April 22, 2004, 11:57:12
Job time : 15 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 22, 2004, 11:52:48 ; Search time 16.5 Seconds
(without alignments)

Title: US-10-620-049-25

Perfect score: 1316
Sequence: 1 DIQMTQTSSLASLGDRVT.....GLLRYANDYWGCGTSTVTSS 247

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 segs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

7

Database : Issued_Patents_AA:*

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*

2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*

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3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_5/ptodata/2/iaa/6B_COMB.pep.*
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4: /cgn2_6/ptodata/2/1aa/6B COMB.rep:*
5: /cgn2_6/ptodata/2/1aa/6B COMB.rep:
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5: /cgh2_6/ptodata/2/1aa/PCINUS COMB.pdf
6: /can2_6/ptodata/2/1aa/backf11eal.pdf
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			ID	Description
	Match	Length	DS		
1	952	72.3	302	1	US-08-121-054C-18
2	952	72.3	302	3	US-08-539-436-18
3	952	72.3	302	4	US-09-813-659-18
4	952	72.3	302	4	US-09-549-067A-18
5	951	72.3	274	4	US-09-813-659-30
6	951	72.3	274	4	US-09-549-067A-30
7	951	72.3	302	1	US-08-121-054C-30
8	951	72.3	302	3	US-08-539-436-30
9	951	72.3	302	4	US-09-813-659-32
10	951	72.3	302	4	US-09-549-067A-32
11	819	62.2	271	2	US-08-400-115-4
12	812	61.7	355	3	US-08-875-811-41
13	812	61.7	355	3	US-08-875-811-49
14	812	61.7	355	3	US-08-875-811-64
15	812	61.7	358	3	US-08-875-811-45
16	812	61.7	358	3	US-08-875-811-51
17	812	61.7	360	3	US-08-875-811-47
18	812	61.7	379	3	US-08-875-811-43
19	796.5	60.5	240	1	US-08-488-113B-147
20	796.5	60.5	240	1	US-08-477-484B-147
21	796.5	60.5	240	2	US-08-646-360-147
22	796.5	60.5	240	3	US-08-839-755-147
23	796.5	60.5	240	3	US-09-138-389-147
24	796.5	60.5	240	4	US-09-610-838-147
25	796.5	60.5	240	4	US-09-711-485-147
26	793.5	60.3	301	2	US-08-656-906-25
27	793.5	60.3	301	3	US-09-217-847-25

Query Match	Score	DB 1: Length	DB 2: Length
72.3%	952	302	302

[illegible]

ALIGNMENTS

RESULT 1
 US-08-121-054C-18
 ; Sequence 18, Application US/08121054C
 ; Patent NO. 5637481
 ; GENERAL INFORMATION:
 ; APPLICANT: Ledbetter, Jeffrey A.
 ; APPLICANT: Gilliland, Lisa K.
 ; APPLICANT: Hayden, Martha S.
 ; APPLICANT: Linsley, Peter S.
 ; APPLICANT: Bajorath, Jurgen
 ; APPLICANT: Fell, Perry
 ; TITLE OF INVENTION: Expression Vectors Encoding Bispecific
 ; TITLE OF INVENTION: Fusion Proteins and Methods of Producing Biologically
 ; TITLE OF INVENTION: Active Bispecific Fusion Proteins in a Mammalian Cell
 ; NUMBER OF SEQUENCES: 30
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Merchant & Gould
 ; STREET: 11150 Santa Monica Blvd., Suite 400
 ; CITY: Los Angeles
 ; STATE: CA
 ; COUNTRY: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/121,054C
FILING DATE: 13-SEP-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/013,420
FILING DATE: 01-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436.18US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
FORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 302 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
121-054C-18

Best Local Similarity 75.8%; Pred. No. 4.1e-67;
Matches 191; Conservative 14; Mismatches 39; Indels 8; Gaps 3;
QY 1 DIQMTQTSSLSASLGDRVTUSCRASQDIRNYLWYQOKPDGTVKFLIYVTSRLPGVPS 60
Db 24 DIQMTQTSSLSASLGDRVTUSCRASQDIRNYLWYQOKPDGTVKFLIYVTSRLPGVPS 83
QY 61 RFGSGSGTDYSLTINNLEQEDIGTYFCQOQNTLPWTFGGKTLVTKREL 120
Db 84 RFGSGSGTDYSLTINNLEQEDIGTYFCQOQNTLPWTFGGKTLVTKREL 140
QY 121 GSGGGGGS--EVLOQSGPELVKPGASVKISCKDSGYAFNSWVWVQKPGQGLEWIGR 178
Db 141 GSGGGGGSIDEVLOQSGPELVKPGASMTMSCKASGYSFTGYIVNWLKQSHGNLEWIGL 200
QY 179 IYPGDSNNGKFEKAILTADKSSSTAYMOLSLTSDSAVYFCARSGLL---RYAMD 235
Db 201 INPWKGLTYNQKFKGKATLTVDKSSSTAYMOLSLTSDSAVYFCARSGLL---RYAMD 260
QY 236 YWQGTSTVSS 247
Db 261 VMGAGTCTVSS 272

RESULT 2
US-08-539-436-18
; Sequence 18, Application US/08539436
; Patent No. 6132992
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Gilliland, Lisa K.
; APPLICANT: Hayden, Martha S.
; APPLICANT: Linsley, Peter S.
; APPLICANT: Bajorath, Jorgen
; APPLICANT: Fell, Perry
; APPLICANT: Gilliland, Lisa K.
; TITLE OF INVENTION: Expression Vectors Encoding Bispecific
; TITLE OF INVENTION: Fusion Proteins and Methods of Producing Biologically
; TITLE OF INVENTION: Active Bispecific Fusion Proteins in a Mammalian Cell
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Blvd., Suite 400
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/539,436
; FILING DATE: 05-OCT-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/121,054
; FILING DATE: 13-SEP-1993
; APPLICATION NUMBER: US 08/013,420
; FILING DATE: 01-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B.
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436.18US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 302 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear

US-08-539-436-18
Query Match 72.3%; Score 952; DB 3; Length 302;
Best Local Similarity 75.8%; Pred. No. 4.1e-67;
Matches 191; Conservative 14; Mismatches 39; Indels 8; Gaps 3;
QY 1 DIQMTQTSSLSASLGDRVTUSCRASQDIRNYLWYQOKPDGTVKFLIYVTSRLPGVPS 60
Db 24 DIQMTQTSSLSASLGDRVTUSCRASQDIRNYLWYQOKPDGTVKFLIYVTSRLPGVPS 83
QY 61 RFGSGSGTDYSLTINNLEQEDIGTYFCQOQNTLPWTFGGKTLVTKREL 120
Db 84 RFGSGSGTDYSLTINNLEQEDIGTYFCQOQNTLPWTFGGKTLVTKREL 140
QY 121 GSGGGGGS--EVLOQSGPELVKPGASVKISCKDSGYAFNSWVWVQKPGQGLEWIGR 178
Db 141 GSGGGGGSIDEVLOQSGPELVKPGASMTMSCKASGYSFTGYIVNWLKQSHGNLEWIGL 200
QY 179 IYPGDSNNGKFEKAILTADKSSSTAYMOLSLTSDSAVYFCARSGLL---RYAMD 235
Db 201 INPWKGLTYNQKFKGKATLTVDKSSSTAYMOLSLTSDSAVYFCARSGLL---RYAMD 260
QY 236 YWQGTSTVSS 247
Db 261 VMGAGTCTVSS 272

RESULT 3
US-09-813-659-18
; Sequence 18, Application US/09813659
; Patent No. 6482919
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden, Martha S.
; APPLICANT: Linsley, Peter S.
; APPLICANT: Bajorath, Jorgen
; APPLICANT: Fell, H. Perry
; APPLICANT: Gilliland, Lisa K.
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING BISPECIFIC FUSION PROTEINS
; TITLE OF INVENTION: AND METHODS OF PRODUCING BIOLOGICALLY ACTIVE BISPECIFIC
; TITLE OF INVENTION: FUSION PROTEINS IN A MAMMALIAN CELL
; FILE REFERENCE: 30436.18USD2
; CURRENT APPLICATION NUMBER: US/09/813,659
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 09/549,067
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 08/539,436
; PRIOR FILING DATE: 1995-10-05
; PRIOR APPLICATION NUMBER: 08/121,054
; PRIOR FILING DATE: 1993-09-13
; PRIOR APPLICATION NUMBER: 08/013,420
; PRIOR FILING DATE: 1993-02-01
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-659-18

Query Match 72.3%; Score 952; DB 4; Length 302;
Best Local Similarity 75.8%; Pred. No. 4.1e-67;
Matches 191; Conservative 14; Mismatches 39; Indels 8; Gaps 3;
QY 1 DIQMTQTSSLSASLGDRVTUSCRASQDIRNYLWYQOKPDGTVKFLIYVTSRLPGVPS 60
Db 24 DIQMTQTSSLSASLGDRVTUSCRASQDIRNYLWYQOKPDGTVKFLIYVTSRLPGVPS 83
QY 61 RFGSGSGTDYSLTINNLEQEDIGTYFCQOQNTLPWTFGGKTLVTKREL 120
Db 84 RFGSGSGTDYSLTINNLEQEDIGTYFCQOQNTLPWTFGGKTLVTKREL 140
QY 121 GSGGGGGS--EVLOQSGPELVKPGASVKISCKDSGYAFNSWVWVQKPGQGLEWIGR 178

Db 141 GSGGGGSDVQLQSGPGLVPGASMTWCKASGYFTGYIVNWLKQSHGNLEWIGL 200
Qy 179 IYPGDGSDNYNGKFEKGAITLADKSSSTAYMQLSSLTVDVSAVYFCARSGLL---RYAMD 235
Db 201 INPKGLTNTNQKFKGKATLTVDKSSSTAYMQLSSLTVDVSAVYFCARSGYGSDWYFD 260
Qy 236 YWGGTSTVTVSS 247
Db 261 VWGAGTTCVTSS 272

RESULT 4
US-09-549-067A-18
; Sequence 18, Application US/09549067A
; Patent No. 6623940
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden, Martha S.
; APPLICANT: Linsley, Peter S.
; APPLICANT: Bajorath, Jurgen
; APPLICANT: Fell, H. Perry
; APPLICANT: Gilliland, Lisa K.
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING BISPECIFIC FUSION PROTEINS
; TITLE OF INVENTION: AND METHODS OF PRODUCING BIOLOGICALLY ACTIVE BISPECIFIC
; TITLE OF INVENTION: FUSION PROTEINS IN A MAMMALIAN CELL
; FILE REFERENCE: 30436.18USC1
; CURRENT APPLICATION NUMBER: US/09/549,067A
; CURRENT FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 08/539,436
; PRIOR FILING DATE: 1995-10-05
; PRIOR APPLICATION NUMBER: 08/121,054
; PRIOR FILING DATE: 1993-09-13
; PRIOR APPLICATION NUMBER: 08/013,420
; PRIOR FILING DATE: 1993-02-01
; PRIOR APPLICATION NUMBER: 08/228,208
; PRIOR FILING DATE: 1994-04-15
; PRIOR APPLICATION NUMBER: 08/008,898
; PRIOR FILING DATE: 1993-01-22
; PRIOR APPLICATION NUMBER: 07/723,617
; PRIOR FILING DATE: 1991-06-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-549-067A-18

Query Match 72.3%; Score 952; DB 4; Length 302;
Best Local Similarity 75.8%; Pred. No. 4.1e-67;
Matches 191; Conservative 14; Mismatches 39; Indels 8; Gaps 3;
Qy 1 DIQMTOTSSLSASLGDRTVSCRASQDIRNLYNQKPDGTVKFLIYVTSRLHPGVPS 60
Db 24 DIQMTOTSSLSASLGDRTVSCRASQDIRNLYNQKPDGTVKFLIYVTSRLHPGVPS 83
Qy 61 RPSGSGSDYSLTINLLEQEDIGTYFCQGNTPMTFGGTVKLEIKRGGSDGGSGG 120
Db 84 RPSGSGSDYSLTINLLEQEDIGTYFCQGNTPMTFGGTVKLEIKRGGSDGGSGG 140
Qy 121 GSGGGGGS--EVQLQSGPELVKPGASVKISCKDGYAFNNSWMNVKQRPQGGLWIGR 178
Db 141 GSGGGGGSIDEVLQSQGPGLVPGASMTWCKASGYFTGYIVNWLKQSHGNLEWIGL 200
Qy 179 IYPGDGSDNYNGKFEKGAITLADKSSSTAYMQLSSLTVDVSAVYFCARSGLL---RYAMD 235
Db 201 INPKGLTNTNQKFKGKATLTVDKSSSTAYMQLSSLTVDVSAVYFCARSGYGSDWYFD 260
Qy 236 YWGGTSTVTVSS 247
Db 261 VWGAGTTCVTSS 272

RESULT 5
US-09-813-659-30
; Sequence 30, Application US/09813659
; Patent No. 6482919
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden, Martha S.
; APPLICANT: Linsley, Peter S.
; APPLICANT: Bajorath, Jurgen
; APPLICANT: Fell, H. Perry
; APPLICANT: Gilliland, Lisa K.
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING BISPECIFIC FUSION PROTEINS
; TITLE OF INVENTION: AND METHODS OF PRODUCING BIOLOGICALLY ACTIVE BISPECIFIC
; TITLE OF INVENTION: FUSION PROTEINS IN A MAMMALIAN CELL
; FILE REFERENCE: 30436.18USD2
; CURRENT APPLICATION NUMBER: US/09/813,659
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 09/549,067
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 08/539,436
; PRIOR FILING DATE: 1995-10-05
; PRIOR APPLICATION NUMBER: 08/121,054
; PRIOR FILING DATE: 1993-09-13
; PRIOR APPLICATION NUMBER: 08/013,420
; PRIOR FILING DATE: 1993-02-01
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-659-30

Query Match 72.3%; Score 951; DB 4; Length 274;
Best Local Similarity 75.8%; Pred. No. 4.4e-67;
Matches 191; Conservative 14; Mismatches 39; Indels 8; Gaps 3;
Qy 1 DIQMTOTSSLSASLGDRTVSCRASQDIRNLYNQKPDGTVKFLIYVTSRLHPGVPS 60
Db 24 DIQMTOTSSLSASLGDRTVSCRASQDIRNLYNQKPDGTVKFLIYVTSRLHPGVPS 83
Qy 61 RPSGSGSDYSLTINLLEQEDIGTYFCQGNTPMTFGGTVKLEIKRGGSDGGSGG 120
Db 84 RPSGSGSDYSLTINLLEQEDIGTYFCQGNTPMTFGGTVKLEIKRGGSDGGSGG 140
Qy 121 GSGGGGGS--EVQLQSGPELVKPGASVKISCKDGYAFNNSWMNVKQRPQGGLWIGR 178
Db 141 GSGGGGGSIDEVLQSQGPGLVPGASMTWCKASGYFTGYIVNWLKQSHGNLEWIGL 200
Qy 179 IYPGDGSDNYNGKFEKGAITLADKSSSTAYMQLSSLTVDVSAVYFCARSGLL---RYAMD 235
Db 201 INPKGLTNTNQKFKGKATLTVDKSSSTAYMQLSSLTVDVSAVYFCARSGYGSDWYFD 260
Qy 236 YWGGTSTVTVSS 247
Db 261 VWGAGTTCVTSS 272

RESULT 6
US-09-549-067A-30
; Sequence 30, Application US/09549067A
; Patent No. 6623940
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden, Martha S.
; APPLICANT: Linsley, Peter S.
; APPLICANT: Bajorath, Jurgen
; APPLICANT: Fell, H. Perry
; APPLICANT: Gilliland, Lisa K.
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING BISPECIFIC FUSION PROTEINS
; TITLE OF INVENTION: AND METHODS OF PRODUCING BIOLOGICALLY ACTIVE BISPECIFIC
; TITLE OF INVENTION: FUSION PROTEINS IN A MAMMALIAN CELL

FILE REFERENCE: 30436.18USC1
CURRENT APPLICATION NUMBER: US/09/549,067A
CURRENT FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: 08/535,436
PRIOR FILING DATE: 1995-10-05
PRIOR APPLICATION NUMBER: 08/121,054
PRIOR FILING DATE: 1993-09-13
PRIOR APPLICATION NUMBER: 08/013,420
PRIOR FILING DATE: 1993-02-01
PRIOR APPLICATION NUMBER: 08/228,208
PRIOR FILING DATE: 1994-04-15
PRIOR APPLICATION NUMBER: 08/008,898
PRIOR FILING DATE: 1993-01-22
PRIOR APPLICATION NUMBER: 07/723,617
PRIOR FILING DATE: 1991-06-27
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 30
LENGTH: 274
TYPE: PRT
ORGANISM: Homo sapiens
US-09-549-067A-30

Query Match 72.3%; Score 951; DB 4; Length 274;
Best Local Similarity 75.8%; Pred. No. 4.4e-67;
Matches 191; Conservative 14; Mismatches 39; Indels 8; Gaps 3;

QY 1 DIQMTOTSSLSASLGDRVTISCRASQDIRNLYNQKPDGTVKFLIYYTSRLLPVPS 60
DB 24 DIQMTOTSSLSASLGDRVTISCRASQDIRNLYNQKPDGTVKFLIYYTSRLHSGVPS 83
QY 61 RFGSGSGTDYSLTINLECEIDIGTYFCQGNTPPWTFGGTKLEIKRGGSGDGGSGG 120
DB 84 RFGSGSGTDYSLTIANLPEDIAITYFCQGNTPPWTFGGTKLVTKRELG---GGSGG 140
QY 121 GSGSGGGS--EVQLQSGPELVKPGASVKISCKDGYAFNNSMMWVKQRPQGLEWIGR 178
DB 141 GSGSGGGSIDEVLQSGPELVKPGASMTMSCASGYSFTGYIVNWLKSHGKLEWIGL 200
QY 179 IYPGDGDSNYNGFEGKAILTADKSSSTAYMQLSSLTSDSAVYFCARSGLL---RYAMD 235
DB 201 INPKGLTITNQKFKGKATLVTKSSSTAYMQLSSLTSDSAVYFCARSGYGGSDWYFD 260
QY 236 YWGQTSVTVSS 247
DB 261 VWGAGTTCVSS 272

RESULT 7
US-08-121-054C-30
Sequence 30, Application US/08121054C
Patent No. 5637481
GENERAL INFORMATION:
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Gilliland, Lisa K.
APPLICANT: Hayden, Martha S.
APPLICANT: Linsley, Peter S.
APPLICANT: Bajorath, Jurgen
APPLICANT: Fell, Perry
TITLE OF INVENTION: Expression Vectors Encoding Bispecific
TITLE OF INVENTION: Fusion Proteins and Methods of Producing Biologically
TITLE OF INVENTION: Active Bispecific Fusion Proteins in a Mammalian Cell
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Blvd., Suite 400
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/121,054C
FILING DATE: 13-SEP-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/013,420
FILING DATE: 01-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436.18US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 302 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-121-054C-30

FILE REFERENCE: 30436.18USC1
CURRENT APPLICATION NUMBER: US/09/549,067A
CURRENT FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: 08/535,436
PRIOR FILING DATE: 1995-10-05
PRIOR APPLICATION NUMBER: 08/121,054
PRIOR FILING DATE: 1993-09-13
PRIOR APPLICATION NUMBER: 08/013,420
PRIOR FILING DATE: 1993-02-01
PRIOR APPLICATION NUMBER: 08/228,208
PRIOR FILING DATE: 1994-04-15
PRIOR APPLICATION NUMBER: 08/008,898
PRIOR FILING DATE: 1993-01-22
PRIOR APPLICATION NUMBER: 07/723,617
PRIOR FILING DATE: 1991-06-27
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 30
LENGTH: 274
TYPE: PRT
ORGANISM: Homo sapiens
US-09-549-067A-30

Query Match 72.3%; Score 951; DB 4; Length 274;
Best Local Similarity 75.8%; Pred. No. 4.4e-67;
Matches 191; Conservative 14; Mismatches 39; Indels 8; Gaps 3;

QY 1 DIQMTOTSSLSASLGDRVTISCRASQDIRNLYNQKPDGTVKFLIYYTSRLLPVPS 60
DB 24 DIQMTOTSSLSASLGDRVTISCRASQDIRNLYNQKPDGTVKFLIYYTSRLHSGVPS 83
QY 61 RFGSGSGTDYSLTINLECEIDIGTYFCQGNTPPWTFGGTKLEIKRGGSGDGGSGG 120
DB 84 RFGSGSGTDYSLTIANLPEDIAITYFCQGNTPPWTFGGTKLVTKRELG---GGSGG 140
QY 121 GSGSGGGS--EVQLQSGPELVKPGASVKISCKDGYAFNNSMMWVKQRPQGLEWIGR 178
DB 141 GSGSGGGSIDEVLQSGPELVKPGASMTMSCASGYSFTGYIVNWLKSHGKLEWIGL 200
QY 179 IYPGDGDSNYNGFEGKAILTADKSSSTAYMQLSSLTSDSAVYFCARSGLL---RYAMD 235
DB 201 INPKGLTITNQKFKGKATLVTKSSSTAYMQLSSLTSDSAVYFCARSGYGGSDWYFD 260
QY 236 YWGQTSVTVSS 247
DB 261 VWGAGTTCVSS 272

RESULT 7
US-08-121-054C-30
Sequence 30, Application US/08121054C
Patent No. 5637481
GENERAL INFORMATION:
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Gilliland, Lisa K.
APPLICANT: Hayden, Martha S.
APPLICANT: Linsley, Peter S.
APPLICANT: Bajorath, Jurgen
APPLICANT: Fell, Perry
TITLE OF INVENTION: Expression Vectors Encoding Bispecific
TITLE OF INVENTION: Fusion Proteins and Methods of Producing Biologically
TITLE OF INVENTION: Active Bispecific Fusion Proteins in a Mammalian Cell
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Blvd., Suite 400
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

```

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/539,436
; FILING DATE: 05-OCT-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/121,054
; FILING DATE: 13-SEP-1993
; APPLICATION NUMBER: US 08/013,420
; FILING DATE: 01-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B.
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436.18US01
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 302 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-539-436-30

Query Match 72.3%; Score 951; DB 3; Length 302;
Best Local Similarity 75.8%; Pred. No. 4.9e-67;
Matches 191; Conservative 14; Mismatches 39; Indels 8; Gaps 3;

QY 1 DIQMTQTSSLSASLGRVTVSCRASQDIRNLYNWYQKPDGTGTVKFLIYVTSRLPGVPS 60
DB 24 DIQMTQTSSLSASLGRVTVSCRASQDIRNLYNWYQKPDGTGTVKFLIYVTSRLHSGVPS 83
QY 61 RFGSGSGTDYSLTINNLEOEDIGTYFCQGNTPPWTFGGGTLKLEIKRGGSGDGGSGG 120
DB 84 RFGSGSGTDYSLTIANLQPEDIATYFCQGNTPPWTFGGGTLKLVTKRELGL--GGSGG 140
QY 121 GSGSGGGS--EVQLQQSGPELVKPGASVKISCKDQSGYAFNNSWMNVKQRPQGLEWIGR 178
DB 141 GSGSGGGSIDEVQLQQSGPELVKPGASVTMSCKASGYSFTGYIYNWLKQSHGNLEWIGL 200
QY 179 IYPGDSNNGKPFEGKAILTADKSSSTAYWQLSLSVDSAVYFCARSGLL---RYAMD 235
DB 201 INFYKGLTINYKQKFGKATLVDKSSSTAYWQLSLSVDSAVYFCARSGYGDSDWYFD 260
QY 236 YMGQGTSTVSS 247
DB 261 VVGAGTTCVSS 272

RESULT 9
US-09-813-659-32
; Sequence 32, Application US/09813659
; Patent No. 6482919
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden, Martha S.
; APPLICANT: Linsley, Peter S.
; APPLICANT: Bajorath, Jurgen
; APPLICANT: Fell, H. Perry
; APPLICANT: Gilliland, Lisa K.
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING BISPECIFIC FUSION PROTEINS
; TITLE OF INVENTION: AND METHODS OF PRODUCING BIOLOGICALLY ACTIVE BISPECIFIC
; TITLE OF INVENTION: FUSION PROTEINS IN A MAMMALIAN CELL
; FILE REFERENCE: 30436.18USD1
; CURRENT APPLICATION NUMBER: US/09/813,659
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 09/549,067
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 08/539,436
; PRIOR FILING DATE: 1995-10-05
; PRIOR APPLICATION NUMBER: 08/121,054
; PRIOR FILING DATE: 1993-09-13
; PRIOR APPLICATION NUMBER: 08/013,420
; PRIOR FILING DATE: 1993-02-01
; PRIOR APPLICATION NUMBER: 08/228,208
; PRIOR FILING DATE: 1994-04-15
; PRIOR APPLICATION NUMBER: 08/008,898
; PRIOR FILING DATE: 1993-01-22
; PRIOR APPLICATION NUMBER: 07/723,617
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-549-067A-32

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; PRIOR APPLICATION NUMBER: 08/121,054
; PRIOR FILING DATE: 1993-09-13
; PRIOR APPLICATION NUMBER: 08/013,420
; PRIOR FILING DATE: 1993-02-01
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-813-659-32

Query Match 72.3%; Score 951; DB 4; Length 302;
Best Local Similarity 75.8%; Pred. No. 4.9e-67;
Matches 191; Conservative 14; Mismatches 39; Indels 8; Gaps 3;

QY 1 DIQMTQTSSLSASLGRVTVSCRASQDIRNLYNWYQKPDGTGTVKFLIYVTSRLPGVPS 60
DB 24 DIQMTQTSSLSASLGRVTVSCRASQDIRNLYNWYQKPDGTGTVKFLIYVTSRLHSGVPS 83
QY 61 RFGSGSGTDYSLTINNLEOEDIGTYFCQGNTPPWTFGGGTLKLEIKRGGSGDGGSGG 120
DB 84 RFGSGSGTDYSLTIANLQPEDIATYFCQGNTPPWTFGGGTLKLVTKRELGL--GGSGG 140
QY 121 GSGSGGGS--EVQLQQSGPELVKPGASVKISCKDQSGYAFNNSWMNVKQRPQGLEWIGR 178
DB 141 GSGSGGGSIDEVQLQQSGPELVKPGASVTMSCKASGYSFTGYIYNWLKQSHGNLEWIGL 200
QY 179 IYPGDSNNGKPFEGKAILTADKSSSTAYWQLSLSVDSAVYFCARSGLL---RYAMD 235
DB 201 INFYKGLTINYKQKFGKATLVDKSSSTAYWQLSLSVDSAVYFCARSGYGDSDWYFD 260
QY 236 YMGQGTSTVSS 247
DB 261 VVGAGTTCVSS 272

RESULT 10
US-09-549-067A-32
; Sequence 32, Application US/09549067A
; Patent No. 6623940
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden, Martha S.
; APPLICANT: Linsley, Peter S.
; APPLICANT: Bajorath, Jurgen
; APPLICANT: Fell, H. Perry
; APPLICANT: Gilliland, Lisa K.
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING BISPECIFIC FUSION PROTEINS
; TITLE OF INVENTION: AND METHODS OF PRODUCING BIOLOGICALLY ACTIVE BISPECIFIC
; TITLE OF INVENTION: FUSION PROTEINS IN A MAMMALIAN CELL
; FILE REFERENCE: 30436.18USC1
; CURRENT APPLICATION NUMBER: US/09/549,067A
; CURRENT FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 08/539,436
; PRIOR FILING DATE: 1995-10-05
; PRIOR APPLICATION NUMBER: 08/121,054
; PRIOR FILING DATE: 1993-09-13
; PRIOR APPLICATION NUMBER: 08/013,420
; PRIOR FILING DATE: 1993-02-01
; PRIOR APPLICATION NUMBER: 08/228,208
; PRIOR FILING DATE: 1994-04-15
; PRIOR APPLICATION NUMBER: 08/008,898
; PRIOR FILING DATE: 1993-01-22
; PRIOR APPLICATION NUMBER: 07/723,617
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-549-067A-32

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Query Match 72.3%; Score 951; DB 4; Length 302;
Best Local Similarity 75.8%; Pred. No. 4.9e-67;
Matches 191; Conservative 14; Mismatches 39; Indels 8; Gaps 3;

QY 1 DIQMTQTSSLSASLGRVTVSCRASQDIRNYLNWYQKPDGTVKFLIYTSRLLPGVPS 60
DB 24 DIQMTQTSSLSASLGRVTVSCRASQDIRNYLNWYQKPDGTVKFLIYTSRLHSGVPS 83

QY 61 RPSGSGGTDSLNNLEQEDICTYFCQOQNTPTWTFGGTKEIKRGGGSDGGSGG 120
DB 84 RPSGSGGTDSLNNLEQEDICTYFCQOQNTPTWTFGGTKEIKRGGGSDGGSGG 140

QY 121 GSGGGGGS--EVQLQQSGPELVKPGASVKISCKDSGYAFNNSMNNWYKQPGGLEWIGR 178
DB 141 GSGGGGGSIDEVQLQQSGPELVKPGASMTMCKASGYFTGIYVNNLKGSHKQKLEWIGL 200

QY 179 IYPGDGSNNGKFEKGAIIADKSSSTAYNQLSSLTSDSAVYFCARSGLL---RYAND 235
DB 201 INPYKGLTYNQKFKGKATLTVDKSSSTAYNQLSSLTSDSAVYFCARSGLSDWYFD 260

QY 236 YVQGTSTVTSS 247
DB 261 VWGAGTCTVSS 272

RESULT 11
US-08-400-115-4
; Sequence 4, Application US/08400115
; Patent No. 5864019
; GENERAL INFORMATION:
; APPLICANT: KING, David John
; APPLICANT: MOUNTAIN, Andrew
; APPLICANT: OWENS, Raymond John
; APPLICANT: YARRANTON, Geoffrey Thomas
; TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/400,115
; FILING DATE: 06-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/127,136
; FILING DATE: 27-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/842,193
; FILING DATE: 17-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/00935
; FILING DATE: 11-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9012995.8
; FILING DATE: 11-JUN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: ISACSON, John P.
; REGISTRATION NUMBER: 33,715
; REFERENCE/DOCKET NUMBER: 040283/0106 CARA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:

LENGTH: 271 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-400-115-4

Query Match 62.2%; Score 819; DB 2; Length 271;
Best Local Similarity 65.6%; Pred. No. 9e-57;
Matches 162; Conservative 28; Mismatches 47; Indels 10; Gaps 2;

QY 1 DIQMTQTSSLSASLGRVTVSCRASQDIRNYLNWYQKPDGTVKFLIYTSRLLPGVPS 60
DB 23 DIQMTQSPASLSVSVGETVTITCRASENIYSLNLAWYQKQKSPQLLYAATNLADGVPS 82

QY 61 RPSGSGGTDSLNNLEQEDICTYFCQOQNTPTWTFGGTKEIKRGGGSDGGSGG 120
DB 83 RPSGSGGTDSLNNLEQEDICTYFCQOQNTPTWTFGGTKEIKRGGGSDGGSGG 137

QY 121 GSGGGGGSVQLQQSGPELVKPGASVKISCKDSGYAFNNSMNNWYKQPGGLEWIGRIY 180
DB 138 GSGGGGGSVQLQQSGPELVKPGASVKISCKASGYFTDTHAIHWAKQKPEQGLEWIGYIS 197

QY 181 PGDGSNNGKFEKGAIIADKSSSTAYNQLSSLTSDSAVYFCARSGLLRVAMDYWGQ 240
DB 198 PGNDIKYNEKFKGKATLTADKSSSTAYNQLSSLTSDSAVYFCARSGLLRVAMDYWGQ 252

QY 241 TSVTVSS 247
DB 253 TILTVSS 259

RESULT 12
US-08-875-811-41
; Sequence 41, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:

LENGTH: 355 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-875-811-41

Query Match 61.7%; Score 812; DB 3; Length 355;
 Best Local Similarity 64.8%; Pred. No. 4.2e-56;
 Matches 160; Conservative 33; Mismatches 44; Indels 10; Gaps 2;

QY	1	DIOMTQTSSLSASIGDRVTVSCRASQDIRNLYNWYQOKPDGTGVKFLIYTSRLPGVPS	60
DB	1	DIKMTQSPSSMYASIGERVTFCKASQDINNLCWFQOKPGKSPKTLIYRANRLVDGVP	60
QY	61	RFSGSGSDTSLTNNLEQEDIGTYFCQGNTPPWTFGGTKLEIKRGSGSDGGSGG	120
DB	61	RFSGSGSDTSLTSSLEYEDMGIIYCLQYDEFFYTFGGTKLEIK-----GGSGSG	114
QY	121	GGSGGGSEVOLQSGPBLVPGASVKISCKDSGVAFNSMNNVVKORPGQGLEWIGRIY	180
DB	115	GGSGGGSEVOLQSGTGLARPGASVQMSCKASGYTFSSYWHWIKORPGQGLDWI	174
QY	181	PDGDSNNGKPEKAILTADKSSSTAYMQLSSLTSDVSADVFCARGLRLYANDYWGQ	240
DB	175	PRNSDTIYNPQFKHAKLTAVTSTAYMELNSLTNEDSAVYYCTP----LYYFDSWGQ	230
QY	241	TSVTYSS 247	
DB	231	TTLTVSS 237	

RESULT 13

US-08-875-811-49
 Sequence 49, Application US/08875811
 Patent No. 6045793
 GENERAL INFORMATION:
 APPLICANT: Rybak, Susanna M.
 APPLICANT: Newton, Dianne L.
 APPLICANT: Boque, Luis
 APPLICANT: Wlodawer, Alexander
 TITLE OF INVENTION: Recombinant Ribonuclease Proteins
 NUMBER OF SEQUENCES: 64
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/875,811
 FILING DATE: 19-FEB-1998
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/US97/02588
 FILING DATE: 19-FEB-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/011,800
 FILING DATE: 21-FEB-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Faris, Susan K.
 REGISTRATION NUMBER: 41,739
 REFERENCE/DOCKET NUMBER: 015280-244100US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 49:
 SEQUENCE CHARACTERISTICS:

LENGTH: 355 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-875-811-49

Query Match 61.7%; Score 812; DB 3; Length 355;
 Best Local Similarity 64.8%; Pred. No. 4.2e-56;
 Matches 160; Conservative 33; Mismatches 44; Indels 10; Gaps 2;

QY	1	DIOMTQTSSLSASIGDRVTVSCRASQDIRNLYNWYQOKPDGTGVKFLIYTSRLPGVPS	60
DB	1	DIKMTQSPSSMYASIGERVTFCKASQDINNLCWFQOKPGKSPKTLIYRANRLVDGVP	60
QY	61	RFSGSGSDTSLTNNLEQEDIGTYFCQGNTPPWTFGGTKLEIKRGSGSDGGSGG	120
DB	61	RFSGSGSDTSLTSSLEYEDMGIIYCLQYDEFFYTFGGTKLEIK-----GGSGSG	114
QY	121	GGSGGGSEVOLQSGPBLVPGASVKISCKDSGVAFNSMNNVVKORPGQGLEWIGRIY	180
DB	115	GGSGGGSEVOLQSGTGLARPGASVQMSCKASGYTFSSYWHWIKORPGQGLDWI	174
QY	181	PDGDSNNGKPEKAILTADKSSSTAYMQLSSLTSDVSADVFCARGLRLYANDYWGQ	240
DB	175	PRNSDTIYNPQFKHAKLTAVTSTAYMELNSLTNEDSAVYYCTP----LYYFDSWGQ	230
QY	241	TSVTYSS 247	
DB	231	TTLTVSS 237	

RESULT 14

US-08-875-811-64
 Sequence 64, Application US/08875811
 Patent No. 6045793
 GENERAL INFORMATION:
 APPLICANT: Rybak, Susanna M.
 APPLICANT: Newton, Dianne L.
 APPLICANT: Boque, Luis
 APPLICANT: Wlodawer, Alexander
 TITLE OF INVENTION: Recombinant Ribonuclease Proteins
 NUMBER OF SEQUENCES: 64
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/875,811
 FILING DATE: 19-FEB-1998
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/US97/02588
 FILING DATE: 19-FEB-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/011,800
 FILING DATE: 21-FEB-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Faris, Susan K.
 REGISTRATION NUMBER: 41,739
 REFERENCE/DOCKET NUMBER: 015280-244100US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 64:
 SEQUENCE CHARACTERISTICS:

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;
; LENGTH: 355 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..355
; OTHER INFORMATION: /note= "B6FB[Met-(-1)]SerrOnc"
US-08-875-811-64

Query Match 61.7%; Score 812; DB 3; Length 355;
Best Local Similarity 64.8%; Pred. No. 4.2e-56;
Matches 160; Conservative 33; Mismatches 44; Indels 10; Gaps 2;

QY 1 DIQMTQTSSLSASLGRVTVSCRASQDINRYLNWYQKPDGTVKELIYYTSRLLPGVPS 60
Db 1 DIKMTQSPSSMYASLGERVTFCKASQDINNYLCWFQKPGKSPKTLIYRANRLVDGVPS 60
QY 61 RFGSGSGDYSLTINNLEQEDIGTYFCQGNTPPMTFGGKLEIKRGGSGDGGSGG 120
Db 61 RFGSGSGQDYSLTSSLEVEDMGIYCYQDEFFYTFGGGKLEIK-----GGGSGG 114
QY 121 GSGSGGSEVQLQSQSGTVLARPASVYKISCKDSGYAFNSMNNWVKQRPQGLEWIGRIY 180
Db 115 GSGSGGSEVQLQSQSGTVLARPASVYKISCKDSGYAFNSMNNWVKQRPQGLEWIV 174
QY 181 PGDSDNNGKFEKKAILLTADKSSSTAYMQLSLSVDSAVYFCARSGLLRYANDYWGQ 240
Db 175 PRNSDTIYNPQFKHAKLTAVTSTSTAYMELNSLTNEDSAVYYCTP-----LYYFDSWGQ 230
QY 241 TSVTVSS 247
Db 231 TLTVSS 237

TELECOMMUNICATION INFORMATION:
;
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-875-811-45

Query Match 61.7%; Score 812; DB 3; Length 358;
Best Local Similarity 64.8%; Pred. No. 4.3e-56;
Matches 160; Conservative 33; Mismatches 44; Indels 10; Gaps 2;

QY 1 DIQMTQTSSLSASLGRVTVSCRASQDINRYLNWYQKPDGTVKELIYYTSRLLPGVPS 60
Db 119 DIKMTQSPSSMYASLGERVTFCKASQDINNYLCWFQKPGKSPKTLIYRANRLVDGVPS 178
QY 61 RFGSGSGDYSLTINNLEQEDIGTYFCQGNTPPMTFGGKLEIKRGGSGDGGSGG 120
Db 179 RFGSGSGQDYSLTSSLEVEDMGIYCYQDEFFYTFGGGKLEIK-----GGGSGG 232
QY 121 GSGSGGSEVQLQSQSGTVLARPASVYKISCKDSGYAFNSMNNWVKQRPQGLEWIGRIY 180
Db 233 GSGSGGSEVQLQSQSGTVLARPASVYKISCKDSGYAFNSMNNWVKQRPQGLEWIV 292
QY 181 PGDSDNNGKFEKKAILLTADKSSSTAYMQLSLSVDSAVYFCARSGLLRYANDYWGQ 240
Db 293 PRNSDTIYNPQFKHAKLTAVTSTSTAYMELNSLTNEDSAVYYCTP-----LYYFDSWGQ 348
QY 241 TSVTVSS 247
Db 349 TLTVSS 355
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Search completed: April 22, 2004, 11:57:59
Job time : 17.5 secs

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RESULT 15
US-08-875-811-45
; Sequence 45, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluis
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 22, 2004, 11:45:27 ; Search time 51 Seconds
(without alignments)
1368.416 Million cell updates/sec

Title: US-10-620-049-25
Perfect score: 1316
Sequence: 1 DIQWQTSSLSASLGRVT.....GLLRVANDVWGQTSVTSS 247

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1246	94.7	247	6 AAO27254	Antibody
2	1243	94.5	247	6 AAO27253	Antibody
3	1242	94.4	247	6 AAO27255	Antibody
4	1235	93.8	247	6 AAO27252	Antibody
5	1230	93.5	247	6 AAO27256	Antibody
6	991	75.3	637	5 AAU75365	Diphtheri
7	991	75.3	638	5 AAU75370	Diphtheri
8	991	75.3	656	5 AAU75383	Immunotox
9	991	75.3	657	5 AAU75389	Diphtheri
10	989	75.2	601	3 ABO7461	An immuno
11	989	75.2	601	6 ABG72265	Recombina
12	989	75.2	642	5 AAU75382	Diphtheri
13	989	75.2	642	6 AAO29675	Anti-T ce
14	989	75.2	643	5 AAU75390	Diphtheri
15	989	75.2	643	6 AAO29670	Anti-T ce
16	985.5	74.9	895	5 AAU75369	Diphtheri
17	985.5	74.9	895	5 AAU75368	Diphtheri
18	985.5	74.9	895	5 AAU75374	Diphtheri
19	985.5	74.9	895	6 AAO29673	Anti-T ce
20	985.5	74.9	896	5 AAU75367	Diphtheri
21	985.5	74.9	896	5 AAU75366	Diphtheri
22	985.5	74.9	896	5 AAU75373	Diphtheri
23	985.5	74.9	896	6 AAO29672	Anti-T ce
24	985.5	74.9	896	6 AAO29671	Anti-T ce
25	985.5	74.9	896	6 AAO29676	Anti-T ce

26	985.5	74.9	899	5 AAU75375	Diphtheri
27	985.5	74.9	899	6 AAO29674	Anti-T ce
28	981.5	74.6	652	5 AAU75448	Immunotox
29	956.5	72.7	554	3 AAU50822	Fv-antibo
30	951	72.3	302	2 AAR60206	Bispecifi
31	945	71.8	504	7 ADD25787	Binding d
32	945	71.8	555	7 ADE86039	Anti-CD3
33	924	70.2	562	6 ABE57058	Plasmid p
34	923.5	70.2	531	3 AAU43749	Amino aci
35	914	69.5	271	5 ABG31022	Mouse sin
36	914	69.5	271	7 ADD25451	Binding d
37	890	67.6	251	4 AAB74793	Single ch
38	883	67.6	258	4 AAB74794	Single ch
39	883	67.1	543	7 ADD12876	CD28/mela
40	881	66.9	507	5 AAU73858	8G7C10x4-
41	871	66.2	539	3 AAU50823	Fv-antibo
42	869	66.0	562	6 ABE57059	Plasmid p
43	848.5	64.5	436	3 AAU91026	Apoptobod
44	845	64.2	650	6 ABR62591	Anti-CD7
45	845	64.2	651	6 ABR62590	Anti-CD7

ALIGNMENTS

RESULT 1
AAO27254
ID AAO27254 standard; protein; 247 AA.
XX
AC AAO27254;
XX
DT 17-SEP-2003 (first entry)
XX
DE Antibody 14B7 scFv mutant 1H amino acid sequence.
XX
KW Mouse; murine; affinity-matured recombinant antibody;
KW proteinaceous toxin; Bacillus anthracis protective antigen;
KW antibacterial; gene therapy; vaccine; biological warfare agent;
KW infection; hybridoma; scFv; 14B7; mutant; mutein; 1H.
XX
OS Mus sp.
OS Synthetic.
XX
FH Key
FT Region 1..108 Location/Qualifiers
FT Region 1..23 /label= Light_chain
FT Region /note= "Light chain framework region 1"
FT Region 24..34 /label= LFR1
FT Region /note= "Complementarity determining region L1"
FT Region 35..49 /label= LFR2
FT Region /note= "Light chain framework region 2"
FT Region 50..56 /label= CDR L2
FT Region /note= "Complementarity determining region L2"
FT Misc-difference 55 /note= "Wild-type Gln substituted by Leu"
FT Misc-difference 56 /note= "Wild-type Ser substituted by Pro"
FT Region 57..88 /label= LFR3
FT Region /note= "Light chain framework region 3"
FT Region 89..97 /label= CDR L3
FT Region /note= "Complementarity determining region L3"
FT Region 98..108 /label= LFR4
FT Region /note= "Light chain framework region 4"
FT Misc-difference 107 /note= "Wild-type Lys substituted by Arg"
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FT 178. .194
FT /label= CDR_H2
FT /note= "Complementarity determining region H2"
FT 195. .226
FT /label= HFR3
FT /note= "Heavy chain framework region 3"
FT Misc-difference 207
FT /note= "Wild-type Ala substituted by Glu"
FT 227. .236
FT /label= CDR_H3
FT /note= "Complementarity determining region H3"
FT 237. .247
FT /label= HFR4
FT /note= "Heavy chain framework region 4"
FT WO2003040384-A1.
XX 15-MAY-2003.
XX 05-NOV-2002; 2002WO-US035567.
XX 05-NOV-2001; 2001US-0332849P.
XX (TEXA ) UNIV TEXAS SYSTEM.
XX Georgiou G, Iverson BL, Maynard JA;
XX WPI; 2003-430672/40.
XX New purified affinity-matured recombinant antibody with binding
XX specificity for Bacillus anthracis protective antigen, useful for
XX diagnosing, preventing or treating anthrax or other bacterial infections.
XX Example; Page; 48pp; English.
XX This invention relates a purified affinity-matured recombinant antibody
XX or its portion having binding specificity for a proteinaceous toxin or a
XX Bacillus anthracis protective antigen. The antibody may have an
XX antibacterial activity and may be used in gene therapy or a vaccine.
XX Bacillus anthracis, commonly referred to as was one of the first
XX biological warfare agents to be developed and is now perceived as a major
XX threat worldwide. The composition and methods of the invention may be
XX useful in diagnosing, preventing or treating infections caused by
XX Bacillus anthracis and other bacterial toxins. The present sequence is
XX that of the mouse wild-type anti-protective antigen hybridoma antibody
XX 14B7 scFv mutant 6A, with a synthetic linker (Gly4Ser)4 between the light
XX and heavy chains. This antibody had Leu46Phe, Ser56Pro, Ser18Thr and
XX Ala207Glu substitutions compared to the wild-type sequence (see AAO27252)
XX and was developed in the examples of the specification in order to
XX identify antibodies which had increased binding affinity for the Bacillus
XX anthracis toxin. Note: This sequence does not appear in the specification
XX but was created by the indexer using information given in the examples
XX and figure 4 of the disclosure
XX Sequence 247 AA;
XX
XX Query Match 94.4%; Score 1242; DB 6; Length 247;
XX Best Local Similarity 94.3%; Pred. No. 6.2e-77;
XX Matches 233; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
XX
Qy 1 DIQMTQTSSLSASLGRVTVSCRASQDIIRNLYNWQKPDGVTKFLIYTSRLPGVPS 60
Db 1 DIQMIQTSSLSASLGRVTVSCRASQDIIRNLYNWQKPDGVTKFLIYTSRLPGVPS 60
Qy 61 RFGSGSGGTDSLFINLLEQEDIGTYFCQGNTPPMTFGGTTKLEIKRGGGSDGGSGG 120
Db 61 RFGSGSGGTDSLFINLLEQEDIGTYFCQGNTPPMTFGGTTKLEIKRGGGSDGGSGG 120
Qy 121 GSGGGGSEVOLQSGPGLVKGASVKISCKDSGYAFNSNMWVQRPQGLWIGRIY 180
Db 121 GSGGGGSEVOLQSGPGLVKGASVKISCKDSGYAFNSNMWVQRPQGLWIGRIY 180
Qy 181 PGDGDNYNGKFKGKATLTADKSSSTGYWQLSSLTSDSVYFCARSGLLRYANDYWGQG 240

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Db 181 PGDGDNYNGKFKGKATLTADKSSSTGYWQLSSLTSDSVYFCARSGLLRYANDYWGQG 240
Qy 241 TSVTVSS 247
Db 241 TSVTVSS 247
RESULT 4
AAO27252
ID AAO27252 standard; protein; 247 AA.
XX AAO27252;
XX 17-SEP-2003 (first entry)
XX Antibody 14B7 scFv wild type amino acid sequence.
XX Mouse; murine; affinity-matured recombinant antibody;
XX proteinaceous toxin; Bacillus anthracis protective antigen;
XX antibacterial; gene therapy; vaccine; biological warfare agent;
XX infection; hybridoma; scFv; 14B7.
XX Mus sp.
XX Synthetic.
XX Key
XX Location/Qualifiers
XX Region 1. .108
XX /label= Light_chain
XX Region 1. .23
XX /label= LFR1
XX /note= "Light chain framework region 1"
XX Region 24. .34
XX /label= CDR_L1
XX /note= "Complementarity determining region L1"
XX Region 35. .49
XX /label= LFR2
XX /note= "Light chain framework region 2"
XX Region 50. .56
XX /label= CDR_L2
XX /note= "Complementarity determining region L2"
XX Region 57. .88
XX /label= LFR3
XX /note= "Light chain framework region 3"
XX Region 89. .97
XX /label= CDR_L3
XX /note= "Complementarity determining region L3"
XX Region 98. .108
XX /label= LFR4
XX /note= "Light chain framework region 4"
XX Region 109. .128
XX /label= Linker
XX /note= "(Gly4Ser)4 linker"
XX Region 129. .247
XX /label= Heavy_chain
XX Region 129. .154
XX /label= HFR1
XX /note= "Heavy chain framework region 1"
XX Region 155. .163
XX /label= CDR_H1
XX /note= "Complementarity determining region H1"
XX Region 164. .177
XX /label= HFR2
XX /note= "Heavy chain framework region 2"
XX Region 178. .194
XX /label= CDR_H2
XX /note= "Complementarity determining region H2"
XX Region 195. .226
XX /label= HFR3
XX /note= "Heavy chain framework region 3"
XX Region 227. .236
XX /label= CDR_H3
XX /note= "Complementarity determining region H3"

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FT Region 237..247
FT /label= HFR4
FT /note= "Heavy chain framework region 4"
FN WO2003040384-A1.
XX 15-MAY-2003.
XX 05-NOV-2002; 2002WO-US035567.
XX 05-NOV-2001; 2001US-0332849P.
XX (TEXA) UNIV TEXAS SYSTEM.
XX Georgiou G, Iverson BL, Maynard JA;
XX WPI; 2003-430672/40.
XX New purified affinity-matured recombinant antibody with binding
XX specificity for Bacillus anthracis protective antigen, useful for
XX diagnosing, preventing or treating anthrax or other bacterial infections.
XX Example; Fig 4; 48pp; English.
XX This invention relates a purified affinity-matured recombinant antibody
XX or its portion having binding specificity for a proteinaceous toxin or a
XX Bacillus anthracis protective antigen. The antibody may have an
XX antibacterial activity and may be used in gene therapy or a vaccine.
XX Bacillus anthracis, commonly referred to as was one of the first
XX biological warfare agents to be developed and is now perceived as a major
XX threat worldwide. The composition and methods of the invention may be
XX useful in diagnosing, preventing or treating infections caused by
XX Bacillus anthracis and other bacterial toxins. The present sequence is
XX that of the mouse wild-type anti-protective antigen hybridoma antibody
XX 14B7 scFv, with a synthetic linker (Gly4Ser)4 between the light and heavy
XX chains. This antibody was used for the development of mutant antibodies
XX (see AAO27253-6) which had increased binding affinity for the Bacillus
XX anthracis toxin in the examples of the specification
SQ Sequence 247 AA;
Query Match 93.8%; Score 1235; DB 6; Length 247;
Best Local Similarity 94.3%; Pred. No. 1.9e-76;
Matches 233; Conservative 5; Mismatches 9; Indels 0; Gaps 0;
QY 1 DIQMOTSSLSASLGDRVTVCASQDIRNLNWKQKPDGTVKFLIYYTSRLPGVPS 60
Db 1 DIQMOTSSLSASLGDRVTVCASQDIRNLNWKQKPDGTVKFLIYYTSRLQSGVPS 60
QY 61 RPSGSGSGTDYSLTINLEQEDIGTYFCQQGNTPWTFGGKTLIKRGSGSGSGGSGG 120
Db 61 RPSGSGSGTDYSLTISNQEDIGTYFCQQGNTPWTFGGKTLIKRGSGSGSGGSGG 120
QY 121 GSGGGGSEVQLQDSGPGLVKPFGASVKLSCKDSGYAFNPSMNWVKQRPQGGLWIGRIY 180
Db 121 GSGGGGSEVQLQDSGPGLVKPFGASVKLSCKDSGYAFNPSMNWVKQRPQGGLWIGRIY 180
QY 181 PGDGSNNGKPEFGKAILTADKSSSTAYNQLSSLTVDSDAVYFCARSGLLRYAMDWQGG 240
Db 181 PGDGTNYNGKPKATLTADKSSSTAYNQLSSLTVDSDAVYFCARSGLLRYAMDWQGG 240
QY 241 TSVTVSS 247
Db 241 TSVTVSS 247
RESULT 5
AAO27256
ID AAO27256 standard; protein; 247 AA.
XX
AC AAO27256;
XX
DT 17-SEP-2003 (first entry)

XX Antibody 14B7 scFv mutant L97 amino acid sequence.
XX Mouse; murine; affinity-matured recombinant antibody;
KW proteinaceous toxin; Bacillus anthracis protective antigen;
KW antibacterial; gene therapy; vaccine; biological warfare agent;
XX infection; hybridoma; scFv; 14B7; mutant; mutein; L97.
XX Mus sp.
OS Synthetic.
XX Key
XX Location/Qualifiers
FT Region 1..108
FT /label= Light_chain
FT Region 1..23
FT /label= LFR1
FT /note= "Light chain framework region 1"
FT Region 24..34
FT /label= CDR L1
FT /note= "Complementarity determining region L1"
FT Region 35..49
FT /label= LFR2
FT /note= "Light chain framework region 2"
FT Region 50..56
FT /label= CDR L2
FT /note= "Complementarity determining region L2"
FT Region 57..88
FT /label= LFR3
FT /note= "Light chain framework region 3"
FT Region 89..97
FT /label= CDR L3
FT /note= "Complementarity determining region L3"
FT Region 98..108
FT /label= LFR4
FT /note= "Light chain framework region 4"
FT Region 109..128
FT /label= Linker
FT /note= "(Gly4Ser)4 linker"
FT Region 129..247
FT /label= Heavy_chain
FT Region 129..154
FT /label= HFR1
FT /note= "Heavy chain framework region 1"
FT Region 155..163
FT /label= CDR H1
FT /note= "Complementarity determining region H1"
FT Region 164..177
FT /label= HFR2
FT /note= "Heavy chain framework region 2"
FT Region 178..194
FT /label= CDR H2
FT /note= "Complementarity determining region H2"
FT Region 195..226
FT /label= HFR3
FT /note= "Heavy chain framework region 3"
FT Region 227..236
FT /label= CDR H3
FT /note= "Complementarity determining region H3"
FT Misc-difference 229
FT /note= "Wild-type Leu substituted by Ala"
FT Region 237..247
FT /label= HFR4
FT /note= "Heavy chain framework region 4"
XX WO2003040384-A1.
XX 15-MAY-2003.
XX 05-NOV-2002; 2002WO-US035567.
XX 05-NOV-2001; 2001US-0332849P.
XX (TEXA) UNIV TEXAS SYSTEM.

Db 508 GSGGGGSEVQLQSGPELVKPGASMKISKASGYSFTGTMNWKSHQKLEWMLIN 567
 Qy 181 PGDGSNYNGKPEGKAILTADKSSSTAYMQLSLTSVDSAVYFCARSGLL---RYAMDYV 237
 Db 568 PYKGVSTYNQKFKDKNFTVDKSSSTAYMQLSLTSVDSAVYFCARSGYVDSWYFDVW 627
 Qy 238 GQGTSTVTSS 247
 Db 628 GQGTTLTVFS 637

RESULT 7
 AAU75370
 ID AAU75370 standard; protein; 638 AA.
 XX AC AAU75370;
 XX 23-APR-2002 (first entry)
 XX Diphtheria toxin/UCHT1 immunotoxin fusion protein #6.
 XX Immunotoxin; pseudomonas exotoxin A; ETA; diphtheria toxin; DT;
 KW cystostatic; immunosuppressive; immunostimulant; antidiabetic;
 KW antirheumatic; antiarthritic; anti-HIV; anti-inflammatory;
 KW anti-T cell immunotoxin fusion protein; antibody; UCHT1;
 KW (Gly4Ser)3 linker; T cell leukaemia; lymphoma; graft-versus-host disease;
 KW Fv; autoimmune disease; transplant rejection;
 KW systemic lupus erythematosus; type I diabetes; rheumatoid arthritis;
 KW myasthenia gravis; multiple sclerosis; AIDS;
 KW acquired immunodeficiency syndrome; chronic immunosuppression.
 XX Mus sp.
 OS Corynebacterium diphtheriae.
 OS Synthetic.
 OS Chimeric.
 XX WO200187982-A2.
 XX 22-NOV-2001.
 XX 18-MAY-2001; 2001WO-US016125.
 XX 18-MAY-2000; 2000US-00573797.
 XX (NOVS) NOVARTIS AG.
 XX (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX Neville DM, Thompson JT, Hu H, Woo J, Ma S, Hexham JM, Digan ME;
 XX WPI; 2002-121980/16.
 XX New anti-T cell immunotoxin fusion protein comprising a truncated
 PT diphtheria toxin moiety, a connector, and one single chain Fv of the
 PT variable region of a UCHT1 antibody, useful for treating e.g. autoimmune
 PT diseases.
 XX Claim 19; Page 269-270; 307pp; English.
 XX The invention relates to an anti-T cell immunotoxin fusion protein,
 CC comprising from the amino terminus, a truncated diphtheria toxin moiety,
 CC a connector, and one single chain Fv of the variable region of a UCHT1
 CC antibody. The single chain Fv comprises VL, L, or VH, L is a Gly-Ser
 CC linker, and VL and VH are the variable light and heavy domains of the
 CC anti-CD3 antibody UCHT1. Also included are a nucleic acid encoding the
 CC novel immunotoxin fusion protein, a vector comprising the nucleic acid
 CC and a cell comprising the nucleic acid. The immunotoxin may also be a
 CC pseudomonas endotoxin A (ETA). The immunotoxins are useful for treating T
 CC cell leukaemias or lymphomas, graft-versus-host diseases, and autoimmune
 CC diseases by inducing immune tolerance. The immunotoxin fusion proteins
 CC may be used in vivo to systemically reduce populations of T cells, or ex
 CC vivo to effect T-cell depletion from a treated cell population. The
 CC fusion proteins can be administered to a subject who is or will be a

CC recipient of an allotransplant to prevent or reduce T-cell mediated acute
 CC or chronic transplant rejection of the transplanted allogeneic cells,
 CC tissue or organ in the subject as well as treat other T-cell mediated
 CC diseases such as systemic lupus erythematosus, type I diabetes,
 CC rheumatoid arthritis, myasthenia gravis, multiple sclerosis, infectious
 CC diseases of the immune system (e.g. AIDS (acquired immunodeficiency
 CC syndrome)) and chronic immunosuppression. The present sequence is an
 CC immunotoxin fusion protein of the invention comprising 330 residues from
 CC the N-terminal glycine of mature DT toxin, a (Gly4Ser)3 linker and one
 CC single Fv chain from antibody UCHT1
 XX
 XX Sequence 638 AA;
 Query Match 75.3%; Score 991; DB 5; Length 638;
 Best Local Similarity 78.0%; Pred. No. 1.9e-59;
 Matches 195; Conservative 13; Mismatches 34; Indels 8; Gaps 2;
 QY 1 DIQMTQTSSLSASLGDRVTVCSCASQDIRNYLNWYQKPDGTVKFLIYYTSRLLPGVPS 60
 Db 394 DIQMTQTSSLSASLGDRVTVCSCASQDIRNYLNWYQKPDGTVKFLIYYTSRLHSVPS 453
 QY 61 RESGSGSGDYSLTINNLEQEDIGTYFCQOQNTPTTGGGTLKIKSGGGSDGGSGG 120
 Db 454 KFSGSGSGDYSLTINNLEQEDIGTYFCQOQNTPTTGGGTLKIKRG-----GGSGG 508
 QY 121 GSGSGSGSEVQLQSGPELVKPGASVKISCKDSGAFNSWMNWKQRPQGLEWIGRIY 180
 Db 509 GSGSGSGSEVQLQSGPELVKPGASVKISCKASGYSGFTGYTNWVKQSHGKULEWMLIN 568
 QY 181 PGDGSNYNGKPEGKAILTADKSSSTAYMQLSLTSVDSAVYFCARSGLL---RYAMDYV 237
 Db 569 PYKGVSTYNQKFKDKNFTVDKSSSTAYMQLSLTSVDSAVYFCARSGYVDSWYFDVW 628
 QY 238 GQGTSTVTSS 247
 Db 629 GQGTTLTVFS 638

RESULT 8
 AAU75383
 ID AAU75383 standard; protein; 656 AA.
 XX AC AAU75383;
 XX 23-APR-2002 (first entry)
 XX Immunotoxin fusion protein related sequence #2.
 XX Immunotoxin; pseudomonas exotoxin A; ETA; diphtheria toxin; DT;
 KW cytostatic; immunosuppressive; immunostimulant; antidiabetic;
 KW antirheumatic; antiarthritic; anti-HIV; anti-inflammatory;
 KW anti-T cell immunotoxin fusion protein; antibody; scUCHT1; Fv; CD3;
 KW T cell leukaemia; lymphoma; graft-versus-host disease;
 KW autoimmune disease; transplant rejection; systemic lupus erythematosus;
 KW type I diabetes; rheumatoid arthritis; myasthenia gravis;
 KW multiple sclerosis; AIDS; acquired immunodeficiency syndrome;
 KW chronic immunosuppression.
 XX Unidentified.
 OS WO200187982-A2.
 XX 22-NOV-2001.
 XX 18-MAY-2001; 2001WO-US016125.
 XX 18-MAY-2000; 2000US-00573797.
 XX (NOVS) NOVARTIS AG.
 XX (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX Neville DM, Thompson JT, Hu H, Woo J, Ma S, Hexham JM, Digan ME;

XX WPI; 2002-121980/16.
 XX New anti-T cell immunotoxin fusion protein comprising a truncated
 XX diphtheria toxin moiety, a connector, and one single chain Fv of the
 XX variable region of a UCHL1 antibody, useful for treating e.g. autoimmune
 XX diseases.
 XX Disclosure; Page 282-283; 307pp; English.
 XX
 XX The invention relates to an anti-T cell immunotoxin fusion protein,
 XX comprising from the amino terminus, a truncated diphtheria toxin moiety,
 XX a connector, and one single chain Fv of the variable region of a UCHL1
 XX antibody. The single chain Fv comprises VL, L, or VH, L is a Gly-Ser
 XX linker, and VL and VH are the variable light and heavy domains of the
 XX anti-CD3 antibody UCHL1. Also included are a nucleic acid encoding the
 XX novel immunotoxin fusion protein, a vector comprising the nucleic acid
 XX and a cell comprising the nucleic acid. The immunotoxin may also be a
 XX pseudomonas endotoxin A (ETA). The immunotoxins are useful for treating T
 XX cell leukemias or lymphomas, graft-versus-host diseases, and autoimmune
 XX diseases by inducing immune tolerance. The immunotoxin fusion proteins
 XX may be used in vivo to systemically reduce populations of T cells, or ex
 XX vivo to effect T-cell depletion from a treated cell population. The
 XX fusion proteins can be administered to a subject who is or will be a
 XX recipient of an allotransplant to prevent or reduce T-cell mediated acute
 XX or chronic transplant rejection of the transplanted allogeneic cells,
 XX tissue or organ in the subject as well as treat other T-cell mediated
 XX diseases such as systemic lupus erythematosus, type I diabetes,
 XX rheumatoid arthritis, myasthenia gravis, multiple sclerosis, infectious
 XX diseases of the immune system (e.g. AIDS (acquired immunodeficiency
 XX syndrome)) and chronic immunosuppression. The present sequence is a
 XX protein sequence included in the sequence listing but not mentioned
 XX elsewhere in the specification, associated with the immunotoxin fusion
 XX proteins of the invention
 XX
 XX Sequence 656 AA;
 XX
 XX Query Match 75.3%; Score 991; DB 5; Length 656;
 XX Best Local Similarity 78.0%; Pred. No. 1.9e-59;
 XX Matches 195; Conservative 13; Mismatches 34; Indels 8; Gaps 2;
 XX
 XX 1 DIQMTQTSSLSASLGDRVTVCSCASQDIENLYNQKPDGTGKFLIYTSRLLPVPS 60
 XX 412 DIQMTQTSSLSASLGDRVTVCSCASQDIENLYNQKPDGTGKFLIYTSRLHSVPS 471
 XX
 XX 61 RFGSGSGTDYSLTINLLEQEDIGYFCQGNTPFTWTFGGGKLEIKRGGSGDGGSGG 120
 XX 472 RFGSGSGTDYSLTINLLEQEDIGYFCQGNTPFTWTFGGGKLEIKRGGSGG 526
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 XX 121 GSGGGGSEVQLQSGPELVKPGASVKISKDGSYAFNNSNNWYKQPGGLEWIGRIY 180
 XX 527 GSGGGGSEVQLQSGPELVKPGASVKISKDGSYAFNNSNNWYKQPGGLEWIGRIY 586
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 XX 181 PGDGSNNYKPEGRKAILTADKSSSTAYNQLSLSLTSVDSAVYFCARSGLL---RYAMDY 237
 XX 587 PKGVSTYNNKPKDKATFTVDKSSSTAYNQLSLSLTSVDSAVYFCARSGLL---RYAMDY 646
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 XX 238 GQGTSTVTS 247
 XX 647 GQGTSTVTS 656
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 XX RESULT 9
 XX AAU75389
 XX ID AAU75389 standard; protein; 657 AA.
 XX AC AAU75389;
 XX XX
 XX 23-APR-2002 (first entry)
 XX Diphtheria toxin/UCHL1 immunotoxin fusion protein HisDT390-sFv.
 XX Immunotoxin; pseudomonas exotoxin A; ETA; diphtheria toxin; DT;

KW cytostatic; immunosuppressive; immunostimulant; antidiabetic;
 KW antirheumatic; antiarthritic; anti-HIV; anti-inflammatory;
 KW anti-T cell immunotoxin fusion protein; antibody; UCHL1;
 KW (Gly4Ser)3 linker; T cell leukaemia; lymphoma; graft-versus-host disease;
 KW Fv; autoimmune disease; transplant rejection;
 KW systemic lupus erythematosus; type I diabetes; rheumatoid arthritis;
 KW myasthenia gravis; multiple sclerosis; AIDS; HisDT390-sFv;
 KW acquired immunodeficiency syndrome; chronic immunosuppression.
 XX
 XX Mus sp.
 XX Corynebacterium diphtheriae.
 XX Synthetic.
 XX Chimeric.
 XX
 XX WO200187982-A2.
 XX
 XX 22-NOV-2001.
 XX
 XX 18-MAY-2001; 2001WO-US016125.
 XX
 XX 18-MAY-2000; 2000US-00573797.
 XX
 XX (NOVS) NOVARTIS AG.
 XX (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 XX Neville DM, Thompson JT, Hu H, Woo J, Ma S, Hexham JM, Digan ME;
 XX WPI; 2002-121980/16.
 XX
 XX New anti-T cell immunotoxin fusion protein comprising a truncated
 XX diphtheria toxin moiety, a connector, and one single chain Fv of the
 XX variable region of a UCHL1 antibody, useful for treating e.g. autoimmune
 XX diseases.
 XX
 XX Example 30; Fig 34; 307pp; English.
 XX
 XX The invention relates to an anti-T cell immunotoxin fusion protein,
 XX comprising from the amino terminus, a truncated diphtheria toxin moiety,
 XX a connector, and one single chain Fv of the variable region of a UCHL1
 XX antibody. The single chain Fv comprises VL, L, or VH, L is a Gly-Ser
 XX linker, and VL and VH are the variable light and heavy domains of the
 XX anti-CD3 antibody UCHL1. Also included are a nucleic acid encoding the
 XX novel immunotoxin fusion protein, a vector comprising the nucleic acid
 XX and a cell comprising the nucleic acid. The immunotoxin may also be a
 XX pseudomonas endotoxin A (ETA). The immunotoxins are useful for treating T
 XX cell leukemias or lymphomas, graft-versus-host diseases, and autoimmune
 XX diseases by inducing immune tolerance. The immunotoxin fusion proteins
 XX may be used in vivo to systemically reduce populations of T cells, or ex
 XX vivo to effect T-cell depletion from a treated cell population. The
 XX fusion proteins can be administered to a subject who is or will be a
 XX recipient of an allotransplant to prevent or reduce T-cell mediated acute
 XX or chronic transplant rejection of the transplanted allogeneic cells,
 XX tissue or organ in the subject as well as treat other T-cell mediated
 XX diseases such as systemic lupus erythematosus, type I diabetes,
 XX rheumatoid arthritis, myasthenia gravis, multiple sclerosis, infectious
 XX diseases of the immune system (e.g. AIDS (acquired immunodeficiency
 XX syndrome)) and chronic immunosuppression. The present sequence is an
 XX immunotoxin fusion protein of the invention comprising 390 residues from
 XX the N-terminal glycine of mature DT toxin, a linker and one single Fv
 XX chain from antibody UCHL1, HisDT390-sFv
 XX
 XX Sequence 657 AA;
 XX
 XX Query Match 75.3%; Score 991; DB 5; Length 657;
 XX Best Local Similarity 78.0%; Pred. No. 1.9e-59;
 XX Matches 195; Conservative 13; Mismatches 34; Indels 8; Gaps 2;
 XX
 XX 1 DIQMTQTSSLSASLGDRVTVCSCASQDIENLYNQKPDGTGKFLIYTSRLLPVPS 60
 XX 413 DIQMTQTSSLSASLGDRVTVCSCASQDIENLYNQKPDGTGKFLIYTSRLHSVPS 472
 XX
 XX 61 RFGSGSGTDYSLTINLLEQEDIGYFCQGNTPFTWTFGGGKLEIKRGGSGDGGSGG 120

Db 473 KFSGGSGTGYSLTINLEQEDTATYFCQGNLTLPWTAGTKLEIKRG-----GGSGG 527
Qy 121 GSGGGGSEVQLQSGPELVKPGASVKISCKDGYAFNNSMMWVVKQRPQGGLEWIGRIY 180
Db 528 GSGGGGSEVQLQSGPELVKPGASVKISCKASGYSGFTGMWVKQSHGKNLEWMLIN 587
Qy 181 PGDGSNNGKPEGKAILTADKSSSTAYMQLSSLTSDSAVYFCARSGLL---RYAMDYW 237
Db 588 FYKGVSTYNQKPKDKATLFDVKSSSTAYMQLSSLTSDSAVYFCARSGLL---RYAMDYW 237
Qy 238 GQGTSTVTSS 247
Db 648 GQGTSTVTSS 657

RESULT 10
AAB07461
ID AAB07461 standard; protein; 601 AA.
AC AAB07461;
XX 20-OCT-2000 (first entry)
DE An immunotoxin comprising a CD3 binding domain and PE28.
XX Immunotoxin; CD3-binding domain; Pseudomonas exotoxin A; immune system;
KW scFv(UCHT-1)-PE28; T-cell mediated disease; transplant rejection;
KW host versus graft disease; graft versus host disease;
KW bone marrow transplant.
XX Synthetic.
OS Mus sp.
OS Pseudomonas aeruginosa.
XX Key Location/Qualifiers
FT Region 3..112
FT /note= "variable region of the light chain"
FT Region 128..249
FT /note= "variable region of the heavy chain"
XX WO200041474-A2.
XX 20-JUL-2000.
XX 13-JAN-2000; 2000WO-BF000245.
XX 15-JAN-1999; 99US-00232445.
XX 25-JAN-1999; 99US-00236968.
XX 07-OCT-1999; 99US-00414134.
XX (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX Digan ME, Lake P, Wright RM;
XX WPI; 2000-482739/42.
XX N-PSDB; AAA58773.
XX Recombinant immunotoxin used for prophylaxis and treatment of T-cell mediated diseases e.g. transplantation rejection.
XX Claim 3; Page 60-63; 75pp; English.
XX The present sequence represents a recombinant immunotoxin comprising a CD3-binding domain and a Pseudomonas exotoxin A component. It is designated scFv(UCHT-1)-PE28. The immunotoxins of the invention are used for the prophylaxis or treatment of T-cell mediated diseases or conditions of the immune system. They are also used to condition a patient to be transplanted with cells, or a tissue or an organ of a donor and for the prophylaxis and/or treatment of acute or chronic CC transplantation rejection, host versus graft disease and/or graft versus CC host disease in a patient to undergo a bone marrow transplant, where the

CC CD3-bearing cell population in the patient is depleted and an inoculum comprising isolated bone marrow and/or stem-cell enriched peripheral CC blood cells of the donor treated with immunotoxin is inoculated into the CC patient
XX SQ Sequence 601 AA;
Qy Query Match 75.2%; Score 989; DB 3; Length 601;
Db Best Local Similarity 78.8%; Pred. No. 2.4e-59;
Qy Matches 197; Conservative 12; Mismatches 35; Indels 6; Gaps 3;
Db 1 DIQMTQTSSLSASLGDRVTISCRASQDIRNVLNMYQKPDGTVKFLIYYTSRLPGVPS 60
3 DIQMTQTSSLSASLGDRVTISCRASQDIRNVLNMYQKPDGTVKFLIYYTSRLHSGVPS 62
61 RESGSGGTDYSLTINLEQEDIGTYFCQGNLTLPWTAGTKLEIKRGSGGSGG 120
63 KFSGGSGTGYSLTINLEQEDTATYFCQGNLTLPWTAGTKLEIKRAGGS-GGSGG 121
121 GSGGGGSEVQLQSGPELVKPGASVKISCKDGYAFNNSMMWVVKQRPQGGLEWIGRIY 180
122 G--SGGGSEVQLQSGPELVKPGASVKISCKASGYSGFTGMWVKQSHGKNLEWMLIN 179
181 PGDGSNNGKPEGKAILTADKSSSTAYMQLSSLTSDSAVYFCARSGLL---RYAMDYW 237
180 FYKGVSTYNQKPKDKATLFDVKSSSTAYMQLSSLTSDSAVYFCARSGLL---RYAMDYW 239
238 GQGTSTVTSS 247
240 GAGTTVTSS 249

RESULT 11
AABG72265
ID AABG72265 standard; protein; 601 AA.
AC AABG72265;
XX 06-MAR-2003 (first entry)
DE Recombinant immunotoxin, scFv(UCHT-1)-PE38.
XX Recombinant immunotoxin; scFv(UCHT-1)-PE38; single chain Fv fragment;
KW murine; anti-human CD3-monoclonal antibody binding domain; UCHT-1;
KW Pseudomonas aeruginosa; exotoxin A; ADP-ribosylating; translocation;
KW T-cell mediated disorder; organ transplantation rejection;
KW autoimmune disease; graft versus host disease; bone marrow transplant;
KW acquired immunodeficiency syndrome; AIDS; T-cell leukaemia;
KW T-cell lymphoma; T-cell-mediated autoimmune disease; type I diabetes;
KW systemic lupus erythematosus; rheumatoid arthritis; myasthenia gravis;
KW multiple sclerosis; immunological tolerance; osteoporosis;
KW aplastic anaemia; Gaucher's disease; thalassaemia; mutant; mutein.
XX Mus sp.
OS Pseudomonas aeruginosa.
OS Synthetic.
OS Chimeric.
XX Key Location/Qualifiers
FT Region 3..111
FT /note= "Light chain variable region (VL)"
FT Peptide 112..127
FT /note= "Linker peptide (L)"
FT Region 128..249
FT /note= "Heavy chain variable region (VH)"
FT Peptide 250..254
FT /note= "Connector peptide (C)"
FT Region 255..601
FT /note= "PE38 mutant"
XX US2002142000-A1.
XX 03-OCT-2002.

XX 10-JAN-2000; 2000US-00480236.
XX 10-JAN-2000; 2000US-00480236.
XX (DIGA/) DIGAN M E.
XX (LAKE/) LAKE P.
XX (WRIGHT/) WRIGHT R. M.
XX Digan WE, Lake P, Wright RM;
XX WPI; 2003-155935/15.
XX N-PSDB; ABX14413.
XX Novel recombinant immunotoxin polypeptide useful for treatment or
XX prophylaxis of T-cell mediated disorders or organ transplantation
XX rejection, comprises a CD3-binding domain and a Pseudomonas exotoxin
XX mutant.
XX Claim 17; Fig 15; 58pp; English.
XX The present invention relates to a novel recombinant immunotoxin,
XX scFv(UCHT-1)-PE38, and the polynucleotide sequence encoding it. The
XX recombinant immunotoxin comprising a single chain (sc) Fv fragment of
XX murine anti-human CD3-monoclonal antibody (UCHT-1) binding domain fused
XX to a Pseudomonas aeruginosa exotoxin A (PE38) mutant having ADP-
XX ribosylating and translocation functions but substantially diminished
XX cell-binding ability. The recombinant immunotoxin is useful for the
XX treatment or prophylaxis of T-cell mediated disorders, organ
XX transplantation rejection or autoimmune disease in a patient. For
XX example, scFv(UCHT-1)-PE38 may be used for treatment or prophylaxis
XX against graft versus host disease in a patient undergoing a bone marrow
XX transplant, for the treatment or prophylaxis of transplant rejection in a
XX patient to undergo a bone marrow transplant, or for conditioning a
XX patient to be transplanted with cells, tissue or organ of a donor.
XX scFv(UCHT-1)-PE38 is also useful for treating acquired immunodeficiency
XX syndrome (AIDS), T-cell leukaemias or lymphomas, T-cell-mediated
XX autoimmune disease such as systemic lupus erythematosus, type I diabetes,
XX rheumatoid arthritis, myasthenia gravis, multiple sclerosis, for inducing
XX immunological tolerance, and for treating diseases curable or treatable
XX by bone marrow transplantation, including leukaemias, osteoporosis,
XX aplastic anaemia, Gaucher's disease, and thalassaemia. The present
XX sequence represents recombinant immunotoxin, scFv(UCHT-1)-PE38
XX
XX Sequence 601 AA;
Query Match 75.2%; Score 989; DB 6; Length 601;
Best Local Similarity 78.8%; Pred. No. 2.4e-59;
Matches 197; Conservative 12; Mismatches 35; Indels 6; Gaps 3;
QY 1 DIQMTTSSLSASLGRVTVSCRASQDINRYLNWYQKPDGVTKLIYTTSLRLFGVPS 60
DB 3 DIQMTTSSLSASLGRVTVSCRASQDINRYLNWYQKPDGVTKLIYTTSLRLHSGVPS 62
QY 61 RFGSGSGTDYSLTINNLBOEDIGTYFCQGNTPPWTFCGGTKLEIKRGGGSDGGSGG 120
DB 63 KFGSGSGTDYSLTINLEQEDATYFCQGNTPPWTFCGGTKLEIKRAGGGS-GGGSGG 121
QY 121 GSGSGSGSEVOLQSGPELVKPCASVKISCKDSGYAFNSWNNWKPQCGLEWIGRIY 180
DB 122 G--SGGSEVOLQSGPELVKPCASVKISCKASGYSTGYTNNWQKSGKLEWGLIN 179
QY 181 PGDGDNYNKKFGKAILTKADKSSSTAYMOLSLTSDVSAVYPCARSGLL---RYANDVW 237
DB 180 PYKGVSTYNQKFKATLVKDSSTAYMELLTSDSDVAVYCARSGYVGDSDVFDVW 239
QY 238 GQGTSTVTVSS 247
DB 240 GAGTTTVTVSS 249
RESULT 12
AAU75382

ID XX AAU75382 standard; protein; 642 AA.
AC XX AAU75382;
XX 23-APR-2002 (first entry)
DT Diphtheria toxin/UCHT1 immunotoxin fusion protein DT389.sfv(UCHT1).
XX Immunotoxin; pseudomonas exotoxin A; ETA; diphtheria toxin; DT;
XX cytostatic; immunosuppressive; immunostimulant; antidiabetic;
XX antirheumatic; antiarthritic; anti-HIV; anti-inflammatory;
XX anti-T cell immunotoxin fusion protein; antibody; UCHT1;
XX (Gly4Ser)3 linker; T cell leukaemia; lymphoma; graft-versus-host disease;
XX Fv; autoimmune disease; transplant rejection;
XX systemic lupus erythematosus; type I diabetes; rheumatoid arthritis;
XX myasthenia gravis; multiple sclerosis; AIDS; DT389.sfv(UCHT1);
XX acquired immunodeficiency syndrome; chronic immunosuppression.
XX Mus sp.
OS Corynebacterium diphtheriae.
OS Synthetic.
OS Chimeric.
XX WO200187982-A2.
XX 22-NOV-2001.
XX 18-MAY-2001; 2001WO-US016125.
XX 18-MAY-2000; 2000US-00573797.
XX (NOVS) NOVARTIS AG.
XX (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX Neville DM, Thompson JT, Hu H, Woo J, Ma S, Hexham JM, Digan ME;
XX WPI; 2002-121980/16.
XX N-PSDB; ABK13467.
XX New anti-T cell immunotoxin fusion protein comprising a truncated
XX diphtheria toxin moiety, a connector, and one single chain Fv of the
XX variable region of a UCHT1 antibody, useful for treating e.g. autoimmune
XX diseases.
XX Claim 5; Fig 35; 307pp; English.
XX The invention relates to an anti-T cell immunotoxin fusion protein,
XX comprising from the amino terminus, a truncated diphtheria toxin moiety,
XX a connector, and one single chain Fv of the variable region of a UCHT1
XX antibody. The single chain Fv comprises VL, L, or VH, L is a Gly-Ser
XX linker, and VL and VH are the variable light and heavy domains of the
XX anti-CD3 antibody UCHT1. Also included are a nucleic acid encoding the
XX novel immunotoxin fusion protein, a vector comprising the nucleic acid
XX and a cell comprising the nucleic acid. The immunotoxin may also be a
XX pseudomonas endotoxin A (ETA). The immunotoxins are useful for treating T
XX cell leukaemias or lymphomas, graft-versus-host diseases, and autoimmune
XX diseases by inducing immune tolerance. The immunotoxin fusion proteins
XX may be used in vivo to systemically reduce populations of T cells, or ex
XX vivo to effect T-cell depletion from a treated cell population. The
XX fusion proteins can be administered to a subject who is or will be a
XX recipient of an allotransplant to prevent or reduce T-cell mediated acute
XX or chronic transplant rejection of the transplanted allogeneic cells,
XX tissue or organ in the subject as well as treat other T-cell mediated
XX diseases such as systemic lupus erythematosus, type I diabetes,
XX rheumatoid arthritis, myasthenia gravis, multiple sclerosis, infectious
XX diseases of the immune system (e.g. AIDS (acquired immunodeficiency
XX syndrome)) and chronic immunosuppression. The present sequence is an
XX immunotoxin fusion protein of the invention comprising 389 residues from
XX the N-terminal glycine of mature DT toxin, a (Gly4Ser)3 linker and one
XX single Fv chain from antibody UCHT1, DT389.sfv(UCHT1)
XX Sequence 642 AA;

CC	malignant proliferative disease such as lymphoma or leukaemia in a
CC	subject, in particular T-cell leukaemia, T-cell lymphoma, including T-
CC	cell granular lymphatic leukaemia, aggressive natural killer cell
CC	leukaemia, hairy-cell leukaemia, Sezary syndrome, angioimmunoblastic T-
CC	cell lymphoma, peripheral T-cell lymphoma unspecified, cutaneous T-cell
CC	lymphoma, subcutaneous panniculitis like T-cell lymphoma, and
CC	hepatosplenic gamma/delta T-cell lymphoma. The present sequence is an
CC	example of anti-T cell immunotoxin fusion protein of the invention
XX	
QQ	Sequence 642 AA;
QQ	Query Match 75.2%; Score 989; DB 6; Length 642;
QQ	Best Local Similarity 78.8%; Pred. No. 2.6e-59;
QQ	Matches 197; Conservative 12; Mismatches 35; Indels 6; Gaps 3;
QY	1 DIQMTQTSSLSASLGDRVTVCRAQDIRNYLNWYQKPDGTVKFLIYYTSRLHSGVPS 60
DB	396 DIQMTQTSSLSASLGDRVTVCRAQDIRNYLNWYQKPDGTVKFLIYYTSRLHSGVPS 455
QY	61 RFGSGSGTDYSLTINNLEQEDIGTYFCQGNTPPWTFGGTCKLEIKRGGSGDGGSGG 120
DB	456 KFGSGSGTDYSLTINNLEQEDIGTYFCQGNTPPWTFAGTCKLEIKRAGGS-GGSGG 514
QY	121 GSGSGGSEVQLQSGPELVKPGASVKISKDSGYAFNSNMWVKORPQGLEWIGRIY 180
DB	515 G--SGGSEVQLQSGPELVKPGASMKISCKASGYSFTGYTMNWVKQSHGKNLEWGLIN 572
QY	181 PGDGSNNGKFEKKAITLTADKSSSTAYMQLSLSVDSAVYFCARSGLL--RYAMDYV 237
DB	573 PYKGVSTYNQKPKDKATLTVDKSSSTAYMQLSLSVDSAVYFCARSGYIGSDWYFDW 632
QY	238 GQGTSTVTVSS 247
DB	633 GAGTIVTVSS 642
RESULT 14	
AAU75390	
ID	AAU75390 standard; protein; 643 AA.
XX	AAU75390;
AC	AAU75390;
XX	23-APR-2002 (first entry)
DT	Diphtheria toxin/UCHT1 immunotoxin fusion protein DT389.scFv(UCHT1).
DE	Immunotoxin; pseudomonas exotoxin A; ETA; diphtheria toxin; DT;
XX	cytotoxic; immunosuppressive; immunostimulant; antidiabetic;
KW	anti-rheumatic; antiarthritic; anti-HIV; anti-inflammatory;
KW	anti-T cell immunotoxin fusion protein; antibody; UCHT1;
KW	(Gly4Ser)3 linker; T cell leukaemia; lymphoma; graft-versus-host disease;
KW	Fv; autoimmune disease; transplant rejection;
KW	systemic lupus erythematosus; type I diabetes; rheumatoid arthritis;
KW	myasthenia gravis; multiple sclerosis; AIDS; DT389.scFv(UCHT1);
KW	acquired immunodeficiency syndrome; chronic immunosuppression.
XX	
OS	Mus sp.
OS	Corynebacterium diphtheriae.
OS	Synthetic.
OS	Chimeric.
XX	WO200187982-A2.
PN	22-NOV-2001.
XX	
XX	18-MAY-2001; 2001WO-US016125.
XX	
XX	18-MAY-2000; 2000US-00573797.
XX	
XX	(NOVS) NOVARTIS AG.
PA	(NOVS) NOVARTIS-BEFLINDUNGEN VERW GES MBH.
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.
XX	

CC	malignant proliferative disease such as lymphoma or leukaemia in a
CC	subject, in particular T-cell leukaemia, T-cell lymphoma, including T-
CC	cell granular lymphatic leukaemia, aggressive natural killer cell
CC	leukaemia, hairy-cell leukaemia, Sezary syndrome, angioimmunoblastic T-
CC	cell lymphoma, peripheral T-cell lymphoma unspecified, cutaneous T-cell
CC	lymphoma, subcutaneous panniculitis like T-cell lymphoma, and
CC	hepatosplenic gamma/delta T-cell lymphoma. The present sequence is an
CC	example of anti-T cell immunotoxin fusion protein of the invention
XX	
XX	Sequence 642 AA;
QY	Query Match 75.2%; Score 989; DB 6; Length 642;
DB	Best Local Similarity 78.8%; Pred. No. 2.6e-59;
DB	Matches 197; Conservative 12; Mismatches 35; Indels 6; Gaps 3;
QY	1 DIQMTQTSSLSASLGDRVTVC
DB	396 DIQMTQTSSLSASLGDRVTVC
QY	61 RFGSGSGTDYSLTINNLEQEDIGTYFCQGNTPPWTFGGT
DB	456 KFGSGSGTDYSLTINNLEQEDIGTYFCQGNTPPWTFAGT
QY	121 GGSGGGSEVQLQSGPELVKPGASVKISCKDSGYAFNSNMWVKORPQGLEWIGRIY
DB	515 G--SGGSEVQLQSGPELVKPGASVKISCKASGYSFTGYTMWVKQSHGKNLEWGLIN
QY	181 PGDGSNNGKFEKKAILTADKSSSTAYMQLSLSVDSAVYFCARSGLL---RYAMDYV
DB	573 PYKGVSTYNQKPKDKATLTVDKSSSTAYMQLSLSVDSAVYFCARSGYIGSDWYFDW
QY	238 GQGTSTVTVSS 247
DB	633 GAGTIVTVSS 642
RESULT 14	
AAU75390	
ID	AAU75390 standard; protein; 643 AA.
XX	AAU75390;
AC	AAU75390;
DT	23-APR-2002 (first entry)
DE	Diphtheria toxin/UCHT1 immunotoxin fusion protein DT389.scFv(UCHT1).
XX	Immunotoxin; pseudomonas exotoxin A; ETA; diphtheria toxin; DT;
KW	cytostatic; immunosuppressive; immunostimulant; antidiabetic;
KW	antirheumatic; antiarthritic; anti-HIV; anti-inflammatory;
KW	anti-T cell immunotoxin fusion protein; antibody; UCHT1;
KW	(Gly4Ser)3 linker; T cell leukaemia; lymphoma; graft-versus-host disease;
KW	Fv; autoimmune disease; transplant rejection;
KW	systemic lupus erythematosus; type I diabetes; rheumatoid arthritis;
KW	myasthenia gravis; multiple sclerosis; AIDS; DT389.scFv(UCHT1);
KW	acquired immunodeficiency syndrome; chronic immunosuppression.
XX	
OS	Mus sp.
OS	Corynebacterium diphtheriae.
OS	Synthetic.
OS	Chimeric.
XX	WO200187982-A2.
XX	
PD	22-NOV-2001.
XX	
PF	18-MAY-2001; 2001WO-US016125.
XX	
PR	18-MAY-2000; 2000US-00573797.
XX	
PA	(NOVS) NOVARTIS AG.
PA	(NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.
XX	

CC malignant proliferative disease such as lymphoma or leukaemia in a
CC subject, in particular T-cell leukaemia, T-cell lymphoma, including T-
CC cell granular lymphatic leukaemia, aggressive natural killer cell
CC leukaemia, hairy-cell leukaemia, Sezary syndrome, angioimmunoblastic T-
CC cell lymphoma, peripheral T-cell lymphoma unspecified, cutaneous T-cell
CC lymphoma, subcutaneous panniculitis like T-cell lymphoma, and
CC hepatosplenic gamma/delta T-cell lymphoma. The present sequence is an
CC example of anti-T cell immunotoxin fusion protein of the invention
XX
SQ Sequence 642 AA;

PI Neville DM, Thompson JT, Hu H, Woo J, Ma S, Hexham JM, Digan ME;
 XX WPI; 2002-121980/16.
 XX
 XX New anti-T cell immunotoxin fusion protein comprising a truncated
 PT diphtheria toxin moiety, a connector, and one single chain Fv of the
 PT variable region of a UCHL1 antibody, useful for treating e.g. autoimmune
 PT diseases.
 XX
 XX Claim 7; Fig 34; 307pp; English.
 XX
 XX The invention relates to an anti-T cell immunotoxin fusion protein,
 CC comprising from the amino terminus, a truncated diphtheria toxin moiety,
 CC a connector, and one single chain Fv of the variable region of a UCHL1
 CC antibody. The single chain Fv comprises VL, L, or VH, L is a Gly-Ser
 CC linker, and VL and VH are the variable light and heavy domains of the
 CC anti-CD3 antibody UCHL1. Also included are a nucleic acid encoding the
 CC novel immunotoxin fusion protein, a vector comprising the nucleic acid
 CC and a cell comprising the nucleic acid. The immunotoxin may also be a
 CC pseudomonas endotoxin A (ETA). The immunotoxins are useful for treating T
 CC cell leukemias or lymphomas, graft-versus-host diseases, and autoimmune
 CC diseases by inducing immune tolerance. The immunotoxin fusion proteins
 CC may be used in vivo to systemically reduce populations of T cells, or ex
 CC vivo to effect T-cell depletion from a treated cell population. The
 CC fusion proteins can be administered to a subject who is or will be a
 CC recipient of an allotransplant to prevent or reduce T-cell mediated acute
 CC or chronic transplant rejection of the transplanted allogeneic cells,
 CC tissue or organ in the subject as well as treat other T-cell mediated
 CC diseases such as systemic lupus erythematosus, type I diabetes,
 CC rheumatoid arthritis, myasthenia gravis, multiple sclerosis, infectious
 CC diseases of the immune system (e.g. AIDS (acquired immunodeficiency
 CC syndrome)) and chronic immunosuppression. The present sequence is an
 CC immunotoxin fusion protein of the invention comprising 389 residues from
 CC the N-terminal glycine of mature DT toxin, a (Gly4Ser)3 linker and one
 CC single Fv chain from antibody UCHL1, DT389.scFv (UCHT1)
 XX
 XX Sequence 643 AA;
 SQ
 Query Match 75.2%; Score 989; DB 5; Length 643;
 Best Local Similarity 78.8%; Pred. No. 2.6e-59;
 Matches 197; Conservative 12; Mismatches 35; Indels 6; Gaps 3;
 QY 1 DIQMTQTSSLSASLGRVTVSCRASQDIRNLYNWYQKPDGTVKFLIYVTSRLLPVPS 60
 DB 397 DIQMTQTSSLSASLGRVTVSCRASQDIRNLYNWYQKPDGTVKFLIYVTSRLHSGVPS 456
 QY 61 RFGSGSGTDYSLTINKLEQEDIGTYFCQCGNTLPWTFFGGTKLEIKRGGSGDGGSGG 120
 DB 457 KFGSGSGTDYSLTINKLEQEDIGTYFCQCGNTLPWTFFGGTKLEIKRGGSGDGGSGG 120
 QY 121 GSGSGSGTDYSLTINKLEQEDIGTYFCQCGNTLPWTFFGGTKLEIKRGGSGDGGSGG 515
 DB 516 G--SGGSGSEVOLQSGPELVKPGASVKISCKDSGYAFNSSWMNVKQRPQGLEWIGRIY 180
 QY 181 PGDGSNYNGKFEKAILTADKSSSTAYMQLSSLTSDSAVYFCARSGLL---RYAMDYV 237
 DB 574 PYKGVSTYNGKFKDKATLTVDKSSSTAYMQLSSLTSDSAVYFCARSGLL---RYAMDYV 237
 QY 238 GQGTSTVTVSS 247
 DB 634 GAGTTVTVSS 643
 RESULT 15
 ID AAO29670 standard; protein; 643 AA.
 XX
 XX AAO29670;
 XX
 XX 22-SEP-2003 (first entry)
 XX
 XX Anti-T cell immunotoxin fusion protein #1.

KW Immunotoxin; anti-T cell; fusion protein; chemotherapeutic agent;
 KW diphtheria toxin; pseudomonas toxin; proliferative disease;
 KW T-cell lymphoma; T-cell lymphoma; T-cell granular lymphatic leukaemia;
 KW aggressive natural killer cell leukaemia; hairy-cell leukaemia;
 KW Sezary syndrome; angioimmunoblastic T-cell lymphoma;
 KW cutaneous T-cell lymphoma.
 XX
 XX Unidentified.
 XX
 XX WO2003045429-A2.
 XX
 XX 05-JUN-2003.
 XX
 XX 27-NOV-2002; 2002WO-EP013387.
 XX
 XX 28-NOV-2001; 2001GB-00028510.
 XX
 XX (NOVS) NOVARTIS AG.
 XX (NOVS) NOVARTIS PHARMA GMBH.
 XX
 XX Engel G;
 XX
 XX WPI; 2003-482489/45.
 XX
 XX Combination for treating malignant proliferative disease, e.g. leukemia
 PT and lymphoma, has an anti-T cell immunotoxin fusion protein comprising a
 PT diphtheria/pseudomonas toxin and a targeting moiety, and a
 PT chemotherapeutic agent.
 XX
 XX Claim 7; Page 23-27; 66pp; English.
 XX
 XX The invention relates to a novel combination comprising an anti-T cell
 CC immunotoxin fusion protein and at least one chemotherapeutic agent. The
 CC fusion protein comprises a diphtheria or pseudomonas toxin moiety and a
 CC targeting moiety suitable for targeting the fusion protein to T cells.
 CC The novel combination is useful for preparing pharmaceutical composition
 CC that is useful for delaying the progression of or for the treatment of a
 CC malignant proliferative disease such as lymphoma or leukemia in a
 CC subject, in particular T-cell leukemia, T-cell lymphoma, including T-
 CC cell granular lymphatic leukemia, aggressive natural killer cell
 CC leukemia, hairy-cell leukemia, Sezary syndrome, angioimmunoblastic T-
 CC cell lymphoma, peripheral T-cell lymphoma unspecified, cutaneous T-cell
 CC lymphoma, subcutaneous panniculitis like T-cell lymphoma, and
 CC hepatocellular carcinoma/delta T-cell lymphoma. The present sequence is an
 CC example of anti-T cell immunotoxin fusion protein of the invention
 XX
 XX Sequence 643 AA;
 SQ
 Query Match 75.2%; Score 989; DB 6; Length 643;
 Best Local Similarity 78.8%; Pred. No. 2.6e-59;
 Matches 197; Conservative 12; Mismatches 35; Indels 6; Gaps 3;
 QY 1 DIQMTQTSSLSASLGRVTVSCRASQDIRNLYNWYQKPDGTVKFLIYVTSRLLPVPS 60
 DB 397 DIQMTQTSSLSASLGRVTVSCRASQDIRNLYNWYQKPDGTVKFLIYVTSRLHSGVPS 456
 QY 61 RFGSGSGTDYSLTINKLEQEDIGTYFCQCGNTLPWTFFGGTKLEIKRGGSGDGGSGG 120
 DB 457 KFGSGSGTDYSLTINKLEQEDIGTYFCQCGNTLPWTFFGGTKLEIKRGGSGDGGSGG 515
 QY 121 GSGSGSGTDYSLTINKLEQEDIGTYFCQCGNTLPWTFFGGTKLEIKRGGSGDGGSGG 180
 DB 516 G--SGGSGSEVOLQSGPELVKPGASVKISCKDSGYAFNSSWMNVKQRPQGLEWIGRIY 180
 QY 181 PGDGSNYNGKFEKAILTADKSSSTAYMQLSSLTSDSAVYFCARSGLL---RYAMDYV 237
 DB 574 PYKGVSTYNGKFKDKATLTVDKSSSTAYMQLSSLTSDSAVYFCARSGLL---RYAMDYV 237
 QY 238 GQGTSTVTVSS 247
 DB 634 GAGTTVTVSS 643

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